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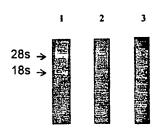
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(54) Title: POLYNUCLEOTIDES AND POLYPEPTIDES



(57) Abstract: The present invention relates to polynucleotide and polypeptide sequences which are associated with eosinophil mediated inflammatory diseases, such as asthma. The invention also relates to means and methods for modulating the expression and/or activity of these sequences, preferably in the treatment or prevention of inflammatory disease mediated by eosinophils. Screening assays for agents which act as agonists or antagonists of these polynucleotides or polypeptides are also provided.

## **POLYNUCLEOTIDES AND POLYPEPTIDES**

# FIELD OF THE INVENTION

- The present invention relates to polynucleotides and polypeptide sequences, and in particular relates to methods and means for the use of these polynucleotide and polypeptide sequences in the diagnosis, prevention and treatment of diseases mediated by eosinophils or other leukocytes, such as inflammatory disease.
- The present invention also relates to the methods and means for modulating the expression and/or activity of such polynucleotides and polypeptides, and to agents which act as agonists or antagonists of these polynucleotides or polypeptides, and methods for identification of such agents.
- The invention also provides oligonucleotide probes and primers, immunoassay kits and methods incorporating these polynucleotides.

## BACKGROUND OF THE INVENTION

Inflammation is an essential protective process preserving the integrity of an organism against 20 physical, chemical and infectious insults. The cellular basis of the inflammation is complex but is, in many cases, dependent on the biological activity of inflammatory leukocytes, including eosinophils [see Gleich G.J. and Adolphson C.R. (1986) The eosinophilic leukocyte, structure and function. Adv. Immunol. 39, 177-253; Giembycz M.A. & Lindsay M.A. (1999) Pharmacol. Rev. 51, 213-339], neutrophils, basophils, mast cells (granulocytes), Tand B -lymphocytes, monocytes 25 and macrophages [see Asthma (1997) Lippencott-Raven, eds Barnes P.J., Grunstein M.M., Leff A.R. & Woolcock A.J.]. Where these cells migrate into the tissues, the key cell/cell interaction is with the vascular endothelium [see Prober J.S. & Cotran R.S. (1990): The role of the endothelum in Inflammation, Transplantation 50, 537-544.] In many cases inappropriate recruitment, proliferation, survival and/or activation of specific leukocytes within a particular 30 organ or tissue will manifest itself as "disease", for example asthma or chronic bronchitis in the lungs, rheumatoid arthritis in the joints or inflammatory bowel disease in the gut. Co-ordination of the inflammatory process is complex and is dependent upon specific gene expression of proteins on the surface of cells to enable cell/cell contact [eg, vascular cell adhesion molecule -1 (VCAM-1) on endothelial cells interacts with the alpha -4 beta- 1 integrin (VLA4) on 35 eosinophils], within the cell to enable intracellular signalling/activation, and within the cell to

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produce inflammatory mediators including eicosanods [Goetzl E.J., An S. & Smith W.I. (1995) FASEB 9, 1051-1058] chemokines and cytokines [ see Arai K-I, Lee F., Miyajima A., Miyatake S., Arai N. & Yokata T (1990) Ann. Rev. Biochemistry 59, 783-836.] Given the range of tissues, cells and mediators involved, the inflammatory response in different disease states has many common features and also many unique features. It is likely that novel genes that are identified from the eosinophil could play an exclusive role in eosinophil biology as it pertains to asthma, but also to other eosinophilic diseases such as atopic dermatitis, hyper-eosinophilic syndrome or pulmonary fibrosis. Novel genes identified in the eosinophil may play other important roles, for example in the biology of other leukocytes; the pathology of inflammatory lung disease other than asthma; or the pathology of any other inflammatory diseases such as rheumatoid arthritis, inflammatory bowel disease (IBD), etc.

Asthma is a chronic inflammatory disease of the airways that is characterised by airway hyperreactivity to exogenous stimuli, inflammatory cell accumulation and airway remodelling. In general terms, asthma causes chronic recurring episodes of coughing, wheezing, chest tightness and difficulty in breathing which can progress to life threatening severity. Exogenous stimuli responsible for precipitating an asthma attack can include airbourne antigens, (pollens, dust mite antigens etc), chemical irritants in pollution, orally derived antigens and other unspecified stimuli. Whilst there is believed to be a genetic predisposition to disease, with an estimated 40-60% heritability, environmental factors undoubtedly play a causal role. Symptomatically the disease can be segmented into intermittent disease with sporadic episodes, persistent disease with mild, moderate and severe severity, and acute severe episodes. Current treatments for asthma range from intermittent bronchodilator therapy (inhaled on demand) to chronic high dose glucocorticosteroids. The use of glucocorticoids in particular is compromised by side effects, notably growth suppression in children that may result from disruption of normal endocrine control of growth and/or a direct effect on bone metabolism in both children or adults. Thus, the identification of novel therapies capable of resolving the chronic inflammatory process without causing side effects would be advantageous. At present many treatments for asthma rely on inhalation delivery. The development of novel, safe, oral therapy with a low frequency of dosing would be particularly advantageous. Many aspects of airway dysfunction are a direct consequence of the underlying airway inflammation that is initiated and sustained by inappropriate proliferation, and/or recruitment and/ or activation of T lymphocytes, B lymphocytes and eosinophils. Asthmatic lungs are characterised by large populations of infiltrating CD4<sup>+</sup> T cells that secrete pro-inflammatory cytokines including IL4, IL13 and IL5. Such T cells are clonally selected by prior exposure to specific antigens and will then respond to secondary antigen exposure with clonal expansion and the production of pro-inflammatory

mediators. However a key characteristic of asthma is systemic and airway eosinophilia. Eosinophils are terminally differentiated leukocytes which make up less than 1% of the leukocyte population in normal individuals and concommitantly trafficking of eosinophils through the normal airways is low. By contrast in asthmatics the circulating levels of eosinophils rises dramatically and can constitute 5-10% of the leukocyte population. Eosinophil myelopoiesis occurs in the bone marrow under the influence of T cell derived cytokines such as IL3, GMCSF and IL5. These circulating eosinophils are actively recruited into the airways by chemoattractants, including chemokines (eotaxin, RANTES) and leukotriene B4. Eosinophils bind to vascular endothelial cells in the airways in an integrin dependent manner and then migrate into the tissues. In normal airways such migrating cells undergo apoptosis and are rapidly cleared, whereas in asthmatics eosinophils are rescued from apoptosis by pro-inflammatory cytokines, including interleukin-5. Together, the increase in availability, recruitment and longevity of eosinophils establishes a tissue eosinophilia in the asthmatic lung. Once resident in the airways eosinophils are activated by a range of pro-inflammatory stimuli including peptido-leukotrienes, platelet activating factor (PAF) complement and sensory neuropetides. Activation causes the eosinphils to release toxic mediators including major basic protein, eosinophil derived neurotoxin and eosinophil cationic protein that are responsible for direct tissue injury notably within the sub-epithelial basement membrane. In addition eosinophils themselves generate proinflammatory cytokines and eicosanoids.

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It is therefore apparent that the eosinophil plays an important causal role in the pathogenisis of inflammatory diseases such as asthma and thus represents an important cellular target for the identification and exploitation of novel drug targets. The most effective anti-inflammatory treatment for asthma which has an impact on eosinophilia is the use of glucocorticosteroids. It is worth noting that the eosinophil, unlike the T cell and the neutrophil is an expendable commodity in normal physiology, given that the normal function of the eosinophil is targetting, killing and expulsion of parasites during chronic parasitic infections.

Another inflammatory disease is COPD (chronic obstructive pulmonary disease) which is characterised by irreversible airway obstruction and encompasses both chronic bronchitis and emphysema. Although COPD has a clinical phenotype and an aetiology that is quite distinct from asthma, as an inflammatory lung disease COPD also has characteristics common to asthma. The major conditions commonly contributing to COPD are chronic bronchitis and emphysema. Changes in airway resistance arises from loss of elastic recoil, narrowing of the distal airways and changes to the airway wall contribute to intrinsic air flow obstruction. The most important risk factor for the development of COPD is cigarette smoking. However it is estimated that only

15% of smokers go on to develop symptoms of COPD. In COPD, lung inflammation predominantly involves neutrophils, interleukin-8 is the cytokine which is most strikingly increased and the increased lymphocytes are type 1 helper T-cells (CD8 T-cells). However the precise role of neutrophils in the lumen of the airways in COPD is not yet established, but it is likely that the release of enzymes such as neutrophil elastase and matrix metalloproteinases (MMP) may contribute to the pathophysiology of the disease. Macrophage numbers are increased by 5-10 times in the airways of patients with COPD and these cells play an important role in driving the inflammatory process by directly producing inflammatory mediators including proteases and neutrophil chemotactic factors. In particular macrophages may be responsible for the continued proteolytic activity observed in the lungs of patients with emphysema. It is likely that some of the novel genes described here may play a role in macrophage or neutrophil biology and as such may play a contributory role in the pathology of COPD. The current therapies for COPD provide modest therapeutic benefit and there are no currently available treatments that influence its progressive cause. In contrast to asthma, COPD is resistant to treatment with glucocorticosteroids and the disease is treated symptomatically with anti-invectives, bronchodiators and mucolytics. Recent data suggest that PDE4 inhibitors may be effective in COPD.

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A number of other diseases have been identified that are associated with hyper-eosinophilia [see Kroegel C,., Warner J.A., Virchow J.C. & Matthys H. (1994) The Eosinophil Leucocyte(partII)Eur. Resp. J. 7, 743-760. These include allergic disorders such as atopic dermatitis and NERDS (nodules eosinophilia, rheumatism, dermatitis and swelling), vasculitic granulomatous diseases including polyarteritis and Wegeners granulomatosis, auto-immune diseases, interstitial and other pulmonary diseases including eosinophilic pneumonia, sarcoiditis and idiopathic pulmonary fibrosis, and neoplastic and myoploriferative diseases including hypereosinophilic syndrome, T cell lymphoma and hodgkins disease.

Thus, there is a need in the art to suppress or inhibit the eosinophil functions that render these leukocytes pivotal in the pathogenesis of inflammatory diseases, particularly asthma. Naturally, such functions are likely to be important in other inflammatory processes involving eosinophils. In particular, there is a need to identify genes that are expressed inappropriately in asthmatics, compared to normals, and which may thus represent suitable targets for pharmaceutical intervention. There is further a need to identify genes encoding proteins that are expressed in normal eosinophils, which regulate eosinophil activation, but that are absent, not expressed normally, or function poorly in asthmatics. There is a particular need to identify genes encoding proteins that affect eosinophil development (myelopocisis), recruitment (adhesion, chemotaxis),

and longevity (e.g. genes involved in apoptosis, or production of chemokines, cytokines, metabolic proteins and toxic secretory proteins). There is also a need to identify genes and gene products that are of diagnostic value, which permit or assist in the diagnosis and differentiation of conditions characterised by inflammation, for example diseases which may cause symptoms such as wheeze, cough, tightness of the chest, breathing difficulties and/or the presence of inflammatory mediators or leukocytes in the airways. There is also a need to identify genes and gene products that are of prognostic value, to assist in the treatment of inflammatory disease such as asthma or which permit different treatments to be evaluated.

- There is also a need to identify genes and gene products that are of therapeutic value, which permit or assist in the treatment of inflammatory disease, such as those characterised by wheeze, cough, tightness of the chest difficulty breathing and/or the presence of inflammatory mediators or leukocytes in the airways.
- There is also a need to identify genes and gene products whose action can be modified to provide new modes of therapeutic intervention, to assist in the treatment and management of inflammatory disease, such as those characterised by wheeze, cough, tightness of the chest difficulty breathing and/or the presence of inflammatory mediators or leukocytes in the airways.

## 20 BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 depicts Gel analysis of RNA isolated using the RNAzol modified methodology (lane 1: Eosinophils, lane 2: Neutrophils, lane 3: Molecular weight marker).

Figure 2 shows the size range of the amplified cDNA which was between 200bp and 7kb.

Figure 3 shows a restriction digest of a cDNA library.

25 Figure 4 shows replacement primers for SMART PCR cDNA synthesis kit.

Figure 5 shows the additional 8bp sites which are used to modify the pSKII (Stratagene) vector.

### **DEFINITIONS**

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The following definitions are provided to facilitate understanding of certain terms used frequently herein:-

In a specific embodiment, the term "about" or "approximately" means within 20%, preferably within 10%, and more preferably within 5% of a given value or range.

"Agonist", as used herein, refers to a molecule which, when bound to a polypeptide of the invention increases or prolongs the duration of the effect of the polypeptide. Agonists may include proteins, nucleic acids, carbohydrates or any other molecules which bind to and modulate the activity of a polypeptide of the invention.

"Amplification", as used herein, relates to the production of additional copies of a nucleic acid sequence. Amplification is generally carried out using polymerase chain reaction (PCR) technologies well known in the art. (See, e.g., Dieffenbach, C.W. and G.S. Dveksler (1995) PCR Primer, a Laboratory Manual, Cold Spring Harbor Press, Plainview, NY, pp. 1-5.)

"Antagonist", as used herein, refers to a molecule which when bound to a polypeptide of the invention decreases the amount or the duration of the effect or the immunological activity of a polypeptide of the invention. Antagonists may include proteins, nucleic acids, carbohydrates, antibodies or any other molecule which decrease the effect of a polypeptide of the invention.

"Autibodies", as used herein, includes polyclonal and monoclonal antibodies, chimeric, single chain, and humanized antibodies as well as Fab fragments, including the products of an Fab or other immunoglobulin expression library.

"Antigenic determinant", as used herein, refers to that fragment of a molecule (i.e. an epitope) that makes contact with a particular antibody. When a protein or a fragment of a protein is used to immunise a host animal, numerous regions of the protein may induce the production of antibodies which bind specifically to antigenic determinants (given regions or three-dimensional structures on the protein). An antigenic determinant may compete with the intact antigen (i.e., the immunogen used to elicit the immune response) for binding to an antibody.

"Antisense", as used herein, refers to any composition containing a nucleic acid sequence which is complementary to a specific nucleic acid sequence. The term "antisense strand" is used in reference to a nucleic acid strand that is complementary to the "sense" strand. Antisense molecules may be produced by any method including synthesis or transcription. Once introduced into a cell, the complementary nucleotides combine with natural sequences produced by the cell to form duplexes and to down regulate or block either transcription or translation. The designation "negative" can refer to the antisense strand, and the designation "positive" can refer to the sense strand.

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"Biologically active", as used herein, refers to a protein having structural, regulatory, or biochemical functions of a naturally occurring molecule. Likewise, "immunologically active" refers to the capability of the natural, recombinant, or synthetic protein, or of any oligopeptide thereof, to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

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"Cassette", as used herein, refers to a segment of DNA that can be inserted into a vector at specific restriction sites. The segment of DNA encodes a polypeptide of interest, and the cassette and restriction sites are designed to ensure insertion of the cassette in the proper reading frame for transcription and translation.

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"Cloning vector", as used herein, is a replicon, such as plasmid, phage or cosmid, to which another DNA segment may be attached so as to bring about the replication of the attached segment. Cloning vectors may be capable of replication in one cell type, and expression in another ("shuttle vector").

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"Coding sequence", as used herein, is a double-stranded DNA sequence which is transcribed and translated into a polypeptide in a cell in vitro or in vivo when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a start codon at the 5' (amino) terminus and a translation stop codon at the 3' (carboxyl) terminus. A coding sequence can include, but is not limited to, prokaryotic sequences, cDNA from eukaryotic mRNA, genomic DNA sequences from eukaryotic (e.g., mammalian) DNA, and even synthetic DNA sequences. If the coding sequence is intended for expression in a eukaryotic cell, a polyadenylation signal and transcription termination sequence will usually be located 3' to the coding sequence.

"Complementary" or "complementarity", as used herein, refer to the natural binding of polynucleotides under permissive salt and temperature conditions by base pairing. For example, the sequence "A-G-T" binds to the complementary sequence "T-C-A."

Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind, or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands. This is of particular importance in amplification reactions, which depend upon binding between nucleic acids strands.

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A "composition comprising a given polynucleotide sequence" or a "composition comprising a given amino acid sequence", as these terms are used herein, refer broadly to any composition containing the given polynucleotide or amino acid sequence. The composition may comprise a dry formulation, an aqueous solution, or a sterile composition. Compositions comprising polynucleotide sequences may be employed as hybridization probes. The probes may be stored in freeze-dried form and may be associated with a stabilising agent such as a carbohydrate. In hybridisation's, the probe may be deployed in an aqueous solution containing salts (e.g NaCl), detergents (e.g., SDS), and other components (e.g., Denhardt's solution, dried milk, salmon sperm DNA, etc.).

"Consensus sequence", as used herein, refers to a nucleic acid sequence which has been resequenced to resolve uncalled bases, extended using XL-PCRTM (Perkin Elmer, Norwalk, CT) in the 5' and/or the 3' direction, and resequenced, or which has been assembled from the overlapping sequences of more than one Clone using a computer program for fragment assembly, such as the GELVIEW<sup>TM</sup>Fragment Assembly system (GCG, Madison, W I). Some sequences have been both extended and assembled to produce the consensus sequence.

The term "corresponding to" is used herein to refer to similar or homologous sequences, whether the exact position is identical or different from the molecule to which the similarity or homology is measured. A nucleic acid or amino acid sequence alignment may include spaces. Thus, the term "corresponding to" refers to the sequence similarity, and not the numbering of the amino acid residues or nucleotide bases.

"Deletion", as the term is used herein, refers to a change in the amino acid or nucleotide sequence that results in the absence of one or more amino acid residues or nucleotides.

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"Derivative", as used herein, refers to the chemical modification of a polynucleotide sequence. Chemical modifications of a polynucleotide sequence can include, for example, replacement of hydrogen by an alkyl, acyl, or amino group. A derivative polynucleotide encodes a polypeptide which retains at least one biological or immunological function of the natural molecule. A derivative polypeptide is one modified by glycosylation, pegylation, or any similar process that retains at least one biological or immunological function of the polypeptide from which it was derived.

"Gene", as used herein, refers to an assembly of nucleotides that encode a polypeptide, and includes cDNA and genomic DNA nucleic acids.

"Heterologous DNA", as used herein, refers to DNA not naturally located in the cell, or in a chromosomal site of the cell. Preferably, the heterologous DNA includes a gene foreign to the cell.

"Heterologous protein", as used herein, refers to a protein not naturally produced in the cell.

"Homologous recombination", as used herein, refers to the insertion of a foreign DNA sequence into another DNA molecule, e.g., insertion of a vector in a chromosome. Preferably, the vector targets a specific chromosomal site for homologous recombination. For specific homologous recombination, the vector will contain sufficiently long regions of homology to sequences of the chromosome to allow complementary binding and incorporation of the vector into the chromosome. Longer regions of homology, and greater degrees of sequence similarity, may increase the efficiency of homologous recombination.

"Homology", as used herein, refers to a degree of complementarity. There may be partial homology or complete homology. The word "identity" may substitute for the word "homology." A partially complementary sequence that at least partially inhibits an identical sequence from hybridising to a target nucleic acid is referred to as "substantially homologous." The inhibition of hybridization of the completely complementary sequence to the target sequence may be examined using a hybridization assay (Southern or Northern blot, solution hybridization, and the like) under conditions of reduced stringency. A substantially homologous sequence or hybridization probe will compete for and inhibit the binding of a completely homologous sequence to the target sequence under conditions of reduced

stringency. This is not to say that conditions of reduced stringency are such that non-specific binding is permitted, as reduced stringency conditions require that the binding of two sequences to one another be a specific (i.e., a selective) interaction. The absence of non-specific binding may be tested by the use of a second target sequence which lacks even a partial degree of complementarity (e.g., less than about 30% homology or identity). In the absence of non-specific binding, the substantially homologous sequence or probe will not hybridise to the second non-complementary target sequence.

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"Human artificial chromosomes (HACs)", as used herein, are linear microchromosomes which may contain DNA sequences of 10K to 10 M in size and contain all of the elements required for stable mitotic chromosome segregation and maintenance (Harrington J.J. et al.(1997) Nat Genet. 15:345-355).

"Hybridization", as used herein, refers to any process by which a strand of nucleic acid binds to another complementary nucleic acid molecule, such as a cDNA, genomic DNA, or RNA, through base pairing. A single stranded form of the nucleic acid molecule can anneal to the other nucleic acid molecule under the appropriate conditions of temperature and solution ionic strength (see Sambrook et al., supra). The conditions of temperature and ionic strength determine the "stringency" of the hybridization. For preliminary screening for homologous nucleic acids, low stringency hybridization conditions, corresponding to a T<sub>m</sub> of 55°, can be used, e.g., 5x SSC, 0.1% SDS, 0.25% milk, and no formamide; or 30% formamide, 5x SSC, 0.5% SDS). Moderate stringency hybridization conditions correspond to a higher Tm, e.g., 40% formamide, with 5x or 6x SCC. High stringency hybridization conditions correspond to the highest  $T_m$ , e.g., 50% formamide, 5x or 6x SCC. Hybridization requires that the two nucleic acids contain complementary sequences, although depending on the stringency of the hybridization, mismatches between bases are possible. The appropriate stringency for hybridising nucleic acids depends on the length of the nucleic acids and the degree of complementation, variables well known in the art. The greater the degree of similarity or homology between two nucleotide sequences, the greater the value of Tm for hybrids of nucleic acids having those sequences. The relative stability (corresponding to higher  $T_m$ ) of nucleic acid hybridizations decreases in the following order: RNA:RNA, DNA:RNA, DNA:DNA. For hybrids of greater than 100 nucleotides in length, equations for calculating  $T_m$  have been derived (see Sambrook et al., supra, 9.50-0.51). For hybridization with shorter nucleic acids, i.e., oligonucleotides, the position of mismatches becomes more important, and the length of the oligonucleotide determines its specificity (see Sambrook et al., supra, 11.7-11.8). Preferably a minimum length for a hybridizable nucleic acid is at least about 10 nucleotides;

preferably at least about 15 nucleotides; and more preferably the length is at least about 20 nucleotides.

"Hybridization complex", as used herein, refers to a complex formed between two nucleic acid sequences by virtue of the formation of hydrogen bonds between complementary bases. A hybridization complex may be formed in solution (e.g., Cot or Rot analysis) or formed between one nucleic acid sequence present in solution and another nucleic acid sequence immobilised on a solid support (e.g., paper, membranes, filters, chips, pins or glass slides, or any other appropriate substrate to which cells or their nucleic acids have been fixed).

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The words "insertion" or "addition", as used herein, refer to changes in an amino acid or nucleotide sequence resulting in the addition of one or more amino acid residues or nucleotides, respectively, to the sequence found in the naturally occurring molecule.

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"Identity" is a measure of the homology of nucleotide sequences or amino acid sequences. In general, the sequences are aligned so that the highest order match is obtained. 'Identity' per se has an art-recognised meaning and can be calculated using published techniques. See, e.g.: (COMPUTATIONAL MOLECULAR BIOLOGY, Losk, A.M., ed., Oxford University Press, New York, 1988; BIOCOMPUTING: INFORMATICS AND GENOME PROJECTS, Smith, D.W., ed., Academic Press, New York, 1993" COMPUTER ANALYSIS OF SEQUENCE DATA, PART 1, Griffin, A.M and Griffin, H.G., eds., Humane Press, New Jersey, 1994; SEQUENCE ANALYSIS IN MOLECULAR BIOLOGY, vol Heinjo, G., Academic Press, 1987; and SEQUENCE ANALYSIS PRIMER, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1 991). While there exist a number of methods to measure identity between two polynucleotide or polypeptide sequences, the term "identity" is well known to skilled artisans (Carillo, H., and Lipton, D., SIAM J AppliadMath (1 988) 48:1073). Methods commonly employed to determine identity or similarity between two sequences include, but are not limited to, those disclosed in Guide to Huge Computers, Martin J. Bishop, ed., Academic Press, San Diego, 1994, and Carillo, H., and Lipton, D., SIAM J Applied Math (1 988) 48:1073. Methods to determine identity and similarity are codified in computer programs. Preferred computer program methods to determine identity and similarity between two sequences include, but are not limited to, GCS program package (Devereux, J., otal., NucloicAcids Research (1984) 12(1):387), BLASTP, BLASTN, FASTA (Atschul, S.F. et al., J Molec Biol(1 990) 215:403). As an illustration, by a polynucleotide having a nucleotide sequence having at least, for example, 95% "identity' to a reference nucleotide sequence of SEO ID NO:l is intended that the nucleotide sequence of the

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polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence of SEQ ID NO: 1. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. These mutations of the reference sequence may occur at the 5' or 3' terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence. Similarly, by a polypeptide having an amino acid sequence having at least, for example, 95% 'identity" to a reference amino acid sequence SEQ ID NO:2 it is intended that the amino acid sequence of the polypeptide is identical to the reference sequence except that the polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the reference amino acid of SEO ID NO: 2. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a reference amino acid sequence, up to 5% of the amino acid residues in the reference sequence may be deleted or substituted with another amino acid, or a number of amino acids up to 5% of the total amino acid residues in the reference sequence may be inserted into the reference sequence. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence. Percent identity or homology is a measure of the relationship between two polypeptide sequences. In general the two sequences to be compared are aligned to give a maximum correlation between the sequences. The alignment of the two sequences is examined and the number of positions giving an exact amino-acid or nucleotide correspondence between the two sequences determined, divided by the total length of the alignment and multiplied by 100 to give a % identity figure. This % identity figure may be determined over the whole length of the sequences to be compared, which is particularly suitable for sequences of the same or very similar length and which are highly homologus, or over shorter defined lengths, which is more suitable for sequences of unequal length or which have a lower level of homology.

"Immune response", as used herein, can refer to conditions associated with inflammation, trauma, immune disorders, or infectious or genetic disease, etc. These conditions can be characterised by expression of various factors, e.g., cytokines, chemokines, and other signalling molecules, which may affect cellular and systemic defence systems.

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"Inflammatory disease" includes disease or conditions which are typically, but not exclusively characterised by wheeze, cough, tightness of chest, breathing difficulties and/or the presence of inflammatory mediators such as leukocytes in the airways.

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"Isolated", as used herein, means altered "by hand of man" from the natural state. If an "isolated" composition or substance occurs in nature, it has been changed or removed from its original environment, or both. For example, a polynucleotide or a polypeptide naturally present in a living animal is not "isolated" but the same polynucleotide or polypeptide separated from the coexisting materials of its natural state is "isolated" as the term is employed herein.

"Microarray", as used herein, refers to an arrangement of distinct polynucleotides arrayed on a substrate, e.g., paper, nylon or any other type of membrane, filter, chip, glass slide, or any other suitable solid support.

"Modulate", as used herein, refers to a change in the activity. For example modulation may cause an increase or a decrease in activity, binding characteristics, or any other biological, functional, or immunological properties and result in tota; inhibition or total activation

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"Nucleic acid", as used herein, is a polymeric compound comprised of covalently linked subunits called nucleotides. Nucleic acid includes polyribonucleic acid (RNA) and polydeoxyribonucleic acid (DNA), both of which may be single-stranded or double-stranded. DNA includes cDNA, genomic DNA, synthetic DNA, and semi-synthetic DNA.

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"Oligonucleotide", as used herein, refers to a nucleic acid sequence, of at least about 6 nucleotides to 60 nucleotides, preferably about 15 to 30 nucleotides, more preferably about 20 to 25 nucleotides, and most preferably at least 18 nucleotides, that is hybridizable to a genomic DNA molecule, a cDNA molecule, or an mRNA molecule. Oligonucleotides can be labelled, e.g., with <sup>32</sup>P-nucleotides or nucleotides to which a label, such as biotin, has been covalently conjugated. In one embodiment, a labelled oligonucleotide can be used as a probe to detect the presence of a nucleic acid. In another embodiment, oligonucleotides (one or both of which may be labelled) can be used as PCR primers, either for cloning full length sequences or fragments thereof, or to detect the presence of specific polynucleotides. In a further embodiment, an oligonucleotide of the invention can form a triple helix with a DNA

molecule. In further embodiments they can be in hybridization assays or microarrays. Generally, oligonucleotides are prepared synthetically, preferably on a nucleic acid synthesiser. Accordingly, oligonucleotides can be prepared with non-naturally occurring phosphoester analog bonds, such as thioester bonds, etc. As used herein, the term "oligonucleotide" is substantially equivalent to the terms "amplimer," "primer," "oligomer," and "probe," as these terms are commonly defined in the art.

"Peptide nucleic acid (PNA)", as used herein, refers to an antisense molecule or anti-gene agent which comprises an oligonucleotide of at least about 5 nucleotides in length linked to a peptide backbone of amino acid residues ending in lysine. The terminal lysine confers solubility to the composition. PNAs preferentially bind complementary single stranded DNA and RNA and stop trandscript elongation, and may be pegylated to extend their lifespan in the cell. (See eg., Nielsen, P. E. et al (1993) Anticancer Drugs Des. 8:53-63).

"Polynucleotide" generally refers to any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. "polynucleotides" include, without limitation single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, 'polynucleotide" refers to triple-stranded regions comprising RNA or DNA or both RNA and DNA. The term polynucleotide also includes DNAs or RNAs containing one or more modified bases and DNAs or RNAs with backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications have been made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically or metabolically modified forms of polynucleotides as typically found in nature, as well as the chemical forms of DNA and RNA characteristic of viruses and cells. "Polynucleotide' also embraces relatively short polynucleotides, often referred to as oligonucleotides.

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"Polypeptide", as used herein, refers to any peptide or protein comprising two or more amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres. "Polypeptide" refers to both short chains, commonly referred to as peptides, oligopeptides or oligomers, and to longer chains, generally referred to as proteins. Polypeptides may contain amino acids other than the 20 gene-encoded amino acids. "Polypeptides' include amino acid sequences modified either by natural processes, such as

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post-translational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in the research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched and branched cyclic polypeptides may result from post-translation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphotidylinositol, cross-linking, cyclization, disulphide bond formation, demethylation, formation of covalent crosslinks, formation of cystine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York, 1993 and Wold, F, Posttransiational Protein Modifications: Perspectives and Prospects, pgs. 1-12 in POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B.C. Johnson, Ed., Academic Press, New York, 1983; Seifter et al., 'Analysis for protein modifications and non-protein cofactors', Meth Enzymol (1990) 182:626-646 and Rattan et al., 'Protein Synthesis: Post-transiational Modifications and Aging', Ann NYAcad Sci (1 992) 663:48-62.

"Probe(s)", as used herein, is a sequence specific polynucleotide or oligonucleotide which is used in the procedure of hybridisation to identify, interogate or probe, a complex mixture of polynucleotides in a sample, or target through sequence specific complimentarity. The probe may be tagged with a label (radioactive, fluorescent or other) as a means to identify complimentary polynucleotides. Alternatively the probe may be attached to, or synthesised on the surface of a chip, slide, filter or other material. In the latter instance the target or sample may be labelled (radioactive, fluorescent or other). The term Probe, is also used to describe the use of an 'electronic' sequence specific polynucleotide or oligonucleotide which is used in the procedure of 'electronic' hybridisation to identify, interogate or probe, a complex mixture

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of 'electronic' polynucleotides in a database or file through sequence specific complimentarity.

"Promoter sequence", as used herein, is a DNA regulatory region capable of binding RNA polymerase in a cell and initiating transcription of a downstream (3' direction) coding sequence. For purposes of defining the present invention, the promoter sequence is bounded at its 3' terminus by the transcription initiation site and extends upstream (5' direction) to include the minimum number of bases or elements necessary to initiate transcription at levels detectable above background. Within the promoter sequence will be found a transcription initiation site (conveniently defined for example, by mapping with nuclease S1), as well as protein binding domains (consensus sequences) responsible for the binding of RNA polymerase.

"Recombinant DNA molecule", as used herein, is a DNA molecule that has undergone a molecular biological manipulation.

"Regulatory region", as used herein, means a nucleic acid sequence which regulates the expression of a second nucleic acid sequence. A regulatory region may include sequences which are naturally responsible for expressing a particular nucleic acid (a homologous region) or may include sequences of a different origin which are responsible for expressing different proteins or even synthetic proteins (a heterologous region). In particular, the sequences can be sequences of eukaryotic or viral genes or derived sequences which stimulate or repress transcription of a gene in a specific or non-specific manner and in an inducible or non-inducible manner. Regulatory regions include origins of replication, RNA splice sites, promoters, enhancers, transcriptional termination sequences, signal sequences which direct the polypeptide into the secretory pathways of the target cell, and promoters.

"Sample", as used herein, may comprise a bodily fluid; an extract from a cell, chromosome, organelle, or membrane isolated from a cell; a cell; genomic DNA, RNA, or cDNA, in solution or bound to a solid support; a tissue; a tissue print; etc.

"Sequence similarity" or "homology", as used herein, refers to the degree of identity or correspondence between nucleic acid or amino acid sequences of proteins that may or may not share a common evolutionary origin (see Reeck et al., supra). However, in common usage and in the instant application, the term "homologous," when modified with an adverb such as "highly," may refer to sequence similarity and not a common evolutionary origin. In a

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specific embodiment, two DNA sequences are "substantially homologous" or "substantially similar" when at least about 50% (preferably at least about 75%, and most preferably at least about 90 or 95%) of the nucleotides match over the defined length of the DNA sequences. Sequences that are substantially homologous can be identified by comparing the sequences using standard software available in sequence data banks, or in a Southern hybridization experiment under, for example, stringent conditions as defined for that particular system. Defining appropriate hybridization conditions is within the skill of the art. See, e.g., Maniatis et al., supra; DNA Cloning, Vols. I & II, supra; Nucleic Acid Hybridization, supra. Two amino acid sequences are "substantially homologous" or "substantially similar" when greater than about 40% of the amino acids are identical, or greater than 60% are similar (functionally identical). Preferably, the similar or homologous sequences are identified by alignment using, for example, the GCG (Genetics Computer Group, Program Manual for the GCG Package, Version 7, Madison, Wisconsin) pileup program.

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"Signal sequence", as used herein, is a sequence included at the beginning of the coding sequence of a protein to be expressed on the surface of a cell. This sequence encodes a signal peptide, N-terminal to the mature polypeptide, that directs the host cell to translocate the polypeptide. The term "translocation signal sequence" is used herein to refer to this sort of signal sequence. Translocation signal sequences can be found associated with a variety of proteins native to eukaryotes and prokaryotes, and are often functional in both types of organisms.

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"Specific binding" or "specifically binding", as used herein, refer to the interaction between a protein or peptide and an agonist, an antibody, or an antagonist. The interaction is dependent upon the presence of a particular structure of the protein, e.g., the antigenic determinant or epitope, recognised by the binding molecule. For example, if an antibody is specific for epitope "A," the presence of a polypeptide containing the epitope A, or the presence of free unlabeled A, in a reaction containing free labelled A and the antibody will reduce the amount of labelled A that binds to the antibody.

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"Standard hybridization conditions", as used herein, refers to a  $T_m$  of 55°C, and utilises conditions as set forth above. In a preferred embodiment, the  $T_m$  is 60°C; in a more preferred embodiment, the  $T_m$  is 65°C

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"Stringent conditions", as used herein, refers to conditions which permit hybridization between polynucleotide sequences and the claimed polynucleotide sequences. Suitably

stringent conditions can be defined by, for example, the concentrations of salt or formamide in the prehybridization and hybridization solutions, or by the hybridization temperature, and are well known in the art. In particular, stringency can be increased by reducing the concentration of salt, increasing the concentration of formamide, or raising the hybridization temperature. For example, hybridization under high stringency conditions could occur in about 50% formainide at about 37'C to 42'C. Hybridization could occur under reduced stringency conditions in about 35% to 25% formamide at about 300C to 35'C. In particular, hybridization could occur under high stringency conditions at 42'C in 50% formamide, 5X SSPE, 0.3% SDS, and 200,ug/ml sheared and denatured salmon sperm DNA. Hybridization could occur under reduced stringency conditions as described above, but in 35% formamide at a reduced temperature of 35°C. The temperature range corresponding to a particular level of stringency can be further narrowed by calculating the purine to pyrimidine ratio of the nucleic acid of interest and adjusting the temperature accordingly. Variations on the above ranges and conditions are well known in the art.

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"Substantially purified", as used herein, refers to nucleic acid or amino acid sequences that are removed from their natural environment and are isolated or separated, and are at least about 60% free, preferably about 75% free, and most preferably about 90% free from other components with which they are naturally associated.

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"Substitution", as used herein, refers to the replacement of one or more amino acids or nucleotides by different amino acids or nucleotides, respectively.

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"Transcriptional control sequences" and "translational control sequences", as used herein, are DNA regulatory sequences, such as promoters, enhancers, terminators, and the like, that provide for the expression of a coding sequence in a host cell. In eukaryotic cells, polyadenylation signals are control sequences. A coding sequence is "under the control" of transcriptional and translational control sequences in a cell when RNA polymerase transcribes the coding sequence into mRNA, which is then trans-RNA spliced (if the coding sequence contains introns) and translated into the protein encoded by the coding sequence.

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"Transfection" by exogenous or heterologous DNA, as used herein, is when such DNA has been introduced inside the cell. A cell has been "transformed" by exogenous or heterologous DNA when the transfected DNA effects a phenotypic change. The transforming DNA can be integrated (covalently linked) into chromosomal DNA making up the genome of the cell.

"Transformation", as defined herein, describes a process by which exogenous DNA enters and changes a recipient cell. Transformation may occur under natural or artificial conditions according to various methods well known in the art, and may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method for transformation is selected based on the type of host cell being transformed and may include, but is not limited to, viral infection, electroporation, heat shock, lipofection, and particle bombardment. The term "transformed" cells includes stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome, as well as transiently transformed cells which express the inserted DNA or RNA for limited periods of time.

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A "variant" of a polynucleotide or a polypeptide, as used herein, is any analogue, fragment, derivative, or mutant which is derived from a different reference polynucleotide or polypeptide and which retains at least one biological property of the reference polynucleotide or polypeptide. Variants of the polypeptide may exist in nature. These variants may be allelic variations characterised by differences in the nucleotide sequences of the structural gene coding for the protein, or may involve differential splicing or post-translational modification. The skilled artisan can produce synthetic polynucleotide or polypeptide variants. Changes in the nucleotide sequence of the variant may or may not alter the amino acid sequence of the polypeptide it encodes. Nucleotide changes may result in amino acid substitutions, additions, deletions, fusions and truncations in the polypeptide it encodes, as discussed below. A typical variant of a polypeptide differs in amino acid sequence from another, reference polypeptide. Generally, differences are limited so that the sequences of the reference polypeptide and the variant are closely similar overall and, in many regions, identical. A variant and reference polypeptide may differ in amino acid sequence by one or more substitutions, additions, replacements or deletions or in any combination thereof. A substituted or inserted amino acid residue may or may not be one encoded by the genetic code. Techniques for obtaining nonnaturally occurring variants of polynucleotides and polypeptides include mutagenesis techniques, genetic (suppressions, deletions, mutations, etc.), chemical, and enzymatic techniques or by direct synthesis all of which are known to persons having ordinary skill in the art. Guidance in determining which amino-acid residues may be substituted inserted or deleted without abolishing biological or immunological activity may be found using computer programs well known in the art such as DNASTAR software.

"Vector", as used herein, is any means for the transfer of a nucleic acid into a host cell. A vector may be a replicon to which another DNA segment may be attached so as to bring about

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the replication of the attached segment. A "replicon" is any genetic element (e.g., plasmid, phage, cosmid, chromosome, virus) that functions as an autonomous unit of DNA replication in vivo, i.e., capable of replication under its own control. The term "vector" includes both viral and nonviral means for introducing the nucleic acid into a cell in vitro, ex vivo or in vivo. Viral vectors include retrovirus, adeno-associated virus, pox, baculovirus, vaccinia, herpes simplex, Epstein-Barr and adenovirus vectors, as set forth in greater detail below. Non-viral vectors include plasmids, liposomes, electrically charged lipids (cytofectins), DNA-protein complexes, and biopolymers. In addition to a nucleic acid, a vector may also contain one or more regulatory regions, and/or selectable markers useful in selecting, measuring, and monitoring nucleic acid transfer results (transfer to which tissues, duration of expression, etc.).

## DESCRIPTION OF THE INVENTION

The present invention is based on the identification and isolation of polynucleotides and polypeptides associated with eosinophil-mediated disease, particularly inflammatory disease such as asthma. The present invention also relates to the use of these polynucleotides and polypeptides in diagnosis, treatment or prevention of diseases mediated by eosinophils, and to the use of oligonucleotides derived from the above polynucleotides and polypeptides as probes or primers for identification of complementary, related or contiguous oligonucleotides or as targets for screening for compounds with pharmaceutical utility or value.

In a first aspect, the present invention relates to polypeptide sequences comprising amino-acid sequences encoded by Seq ID Nos: 1-466 or fragments of those amino acid sequences.

In a preferred embodiment of the first aspect, the invention relates to variants of the amino-acid sequences encoded by Seq ID Nos: 1-466 or fragments of those amino acid sequences, the varients having at least about 80%, more preferably at least 85%, more preferably at least 90%, and most preferably 95% amino-acid sequence identity to the amino-acid sequences encoded by Seq ID Nos: 1-466 or fragments of those amino acid sequences, and which share at least one functional or structural characteristic with the amino-acid sequences encoded by Seq ID Nos: 1-

functional or structural characteristic with the amino-acid sequences encoded by Seq ID Nos: 1-466 or fragments of those amino acid sequences.

In a second aspect the present invention relates to polynucleotide sequences which encode the amino-acid sequences encoded by Seq ID Nos: 1-466 or fragments of those amino acid sequences. Preferably, the polynucleotide sequences of the second aspect are those of Seq ID Nos: 1-466.

In a preferred embodiment of the second aspect, the invention relates to variants of the polynucleotide sequences which encode the amino-acid sequences encoded by Seq ID Nos: 1-466, in particular the polynucleotide sequences of Seq ID Nos: 1-466; or fragments thereof. The variants may have at least about 80%, more preferably at least 85%, more preferably at least 90% and most preferably 95% polynucleotide sequence identity to the polynucleotide sequences which encode the amino-acid sequences encoded by Seq ID Nos: 1-466, in particular the polynucleotide sequences of Seq ID Nos: 1-466. Preferably, the polynucleotide variants described above encode an amino-acid sequence which shares at least one functional and/or structural characteristic with one or more of the amino-acid sequences encoded by Seq ID Nos: 1-466.

As will be appreciated by those skilled in the art, as a result of degeneracy of the genetic code, a multitude of polynucleotide sequences, some bearing minimal homology to the polynucleotide sequence of any known or naturally occurring gene, may be produced. Thus, the invention contemplates each and every possible variation of polynucleotide sequence that could be made by selecting combinations based on possible codon choices. These combinations are made in accordance with the standard triplet genetic code as applied to the naturally occurring polynucleotide sequence, and all such variations are to be considered as being specifically disclosed.

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The polynucleotides of the present invention can be isolated from a number of sources, including genomic libraries, foetal genomic or cDNA libraries, or more preferably from human eosinophil cDNA libraries, preferably constructed from pooled eosinophils harvested from normal or diseased individuals. General methods for obtaining the polynucleotides and polypeptides of the present invention are well known in the art (as described by See, e.g., Sambrook, Fritsch & Maniatis, Molecular Cloning: A Laboratory Manual, Second Edition (1989) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York).

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Genomics techniques were used to study the levels of expression of genes in eosinophils in order to identify the polynucleotides and polypeptides of the present invention which have a role in eosinophil processes which mediate disease. The expression pattern of a gene provides indirect information about its function. A polynucleotide or polypeptide which is selectively expressed in eosinophils is likely to be involved in pathologies associated with the eosinophil, such as asthma, COPD, allergic disorders such as atopic dermatitis and NERDS (nodules eosinophilia, rheumatism, dermatitis and swelling), vasculitic granulomatous diseases including polyarteritis and Wegeners granulomatosis, auto-immune diseases, interstitial and other pulmonary diseases

WO 02/10198 PCT/GB01/03390 22

including eosinophilic pneumonia, sarcoiditis and idiopathic pulmonary fibrosis and neoplastic and myoploriferative diseases including hypereosinophilic syndrome, T cell lymphoma and hodgkins disease. Diversion from normal physiology is frequently accompanied by histological and biochemical changes, including changes in gene expression. The up- or down-regulation of gene activity can either be the cause of the pathophysiology or the result of the disease.

The polynucleotides and polypeptides of the present invention whose modulation results in the modification of eosinophil functions enable for the first time the provision of pharmaceuticals, therapeutic agents, drug targets, gene therapy targets, diagnostic and/or prognostic markers, antibodies which have utility as therapeutic, diagnostic, prognostic, histological or purification tools, and tools for use in the detection and isolation of further polynucleotide or polypeptide sequences which may play a role in eosinophil mediated inflammatory disease.

The identification and/or targetting of polynucleotides and polypeptides according to the first and second aspects of the invention enables the development, duration, progress, outcome, or the damage caused by a disease to be modified, and may even effect a cure. Means and methods for targetting the polynucleotides and/or polypeptides of the present invention may abolish or alleviate one or more symptom of inflammatory disease and/or limit the development, duration, progress, or outcome, of the disease or minimise the damage caused by it. The polynucleotides and polypeptides of the present invention which are not directly responsible for disease may be useful in alleviating or abolishing symptoms associated with the disease.

In particular, the polynucleotides and polypeptides of the present invention may represent attractive targets for drugs. For example, the polynucleotides may be useful targets or agents for gene therapy; the polypeptides may be useful targets for agonists or antagonists which modulate the effects of the polypeptide, and thus mediate a therapeutic effect. In this way, unwanted side effects, symptoms may be alleviated or abolished and causes of the disease may be wholly or partially removed.

Detailed profiling of polynucleotide expression levels in a variety of different tissues in normal and diseased individuals at different stages of disease progression or severity, and in response to a variety of stimuli such as cytokines IL5, drugs, and steroids resulted in the identification of polypeptides and polynucleotides of the present invention. The profiling also enabled indicators of disease stage or progression to be identified, and potential drug targets to be identified.

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Animal disease models enable detailed profiling of gene expression under carefully controlled experimental conditions. For example, the gene expression pattern of a normal animal can be compared against that of a related animal which has been modified in a very specific manner to, such that it either over-or under-expresses one or more selected polynucleotide sequences, or fails to express certain polynucleotide sequences, either because it lacks a functioning copy of the DNA sequence, or because the expression of the sequence has been selectively blocked, for example using antisense oligonucleotides. Such studies provide additional insight into the cellular, animal and human physiology involved in the identification and validation of therapeutic targets.

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Investigations of the expression levels of genes in model cell lines mimicking critical eosinophil functions, such as adhesion, apoptosis, activation, myelopoesis, synthesis of essential cellular components or mediators, and survival, aided the identification of the polynucleotides and polypeptides of the present invention which are expressed or active in the disease causing mechanisms mediated by eosinophils.

Genomics technologies enable many genes to be studied 'in parallel', thereby increasing the chance of identifying a gene or protein which has a key role in diseases mediated by eosinophils. Accordingly, a genomics approach capable of simultaneously analysing the expression levels of large numbers of polynucleotides was utilised to maximise the probability of identifying genes specifically involved in disease processes mediated by eosinophils.

Microarrays to which sequences of interest were applied were used to simultaneously analyse the expression levels of large numbers of polynucleotides. Two microarray technologies for mRNA expression profiling (review: 'The Chipping Forecast', Supplement to Nature Genetics. 21: 1999) were used to investigate/analyse the expression profiles of the polynucleotides of the present invention, one supplied by Affymetrix and the other by Amersham/Molecular Dynamics. Together they offer greater flexibility to generate robust, reproducible and reliable data than either system in isolation.

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The Affymetrix technology, supplied by Affymetrix, U.S.A, comprises microarray chips of high-density oligonucleotides created using adapted photolithographic masking techniques (methodology is as described by the manufacturer; Lockhart, D.J. J. Expression monitoring by hybridisation to high-density oligonucleotide arrays. *Nature Biotechnology*. 14:1675-1680, 1996). A number of different overlapping oligonucleotide pairs corresponding to each polynucleotide sequence to be probed are designed and synthesised (one member of each pair is complementary

to the oligonucleotide sequence of interest and the other, 'control sequence' of the pair includes a single mismatched base). The Affymetrix array system requires prior knowledge of at least a part of each of the nucleotide sequences which are to be attached to the chip to enable suitable probe pairs to be designed and synthesised. This system enables genes of very high homology to be distinguished from one another. This system is very accurate and enables the expression of a large number of genes to be analysed in a single hybridisation reaction. However, once a microarray has been designed and constructed the photolithography process does not allow changes in the nucleotide sequence of the oligonucleotide probes fixed to the array to be made. Accordingly, a new microarray must be designed and synthesised to probe a different set of genes. The array is exposed to labelled cDNA or cRNA from a variety of sources (as described above) under conditions which favour hybridisation. Hybridisation patterns indicate the identity of and the quantity of expression.

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The Amersham Pharmacia Biotechnology/Molecular Dynamics system involves robotically spotting up to 10,000 polynucleotide sequences, normally generated by PCR, onto specially prepared glass slides. It is not necessary to know the nucleotide sequence of the sequences before they are applied to the array. The slide is exposed to fluorescently labelled nucleic acid samples under conditions which favour hybridisation [see Schena, M et al. Quantitative monitoring of gene expression patterns with a complementary DNA microarray. Science 270, 467-470 (1995)]. Hybridisation patterns indicate the identity and the quantity of expression. These microarrays are very flexible and the target fragments applied to the slide can be easily changed. They can be used to determine the differential expression of large numbers of genes, although it is not suitable for those that have high levels of homology to one another.

Several different biological approaches were combined to form an integrated strategy. In the first approach, purified peripheral blood eosinophils were studied from clinically defined normal individuals (e.g. skin test, FEV1, and IgE levels within predefined parameters) and staged asthmatics (e.g. mild, moderate and severe; different values were set for these parameters).

mRNA was isolated from the eosinophils and used to prepare a cDNA library. The mRNA from a number of individuals was pooled to maximise the representation of genes that could be expressed by an eosinophil in different circumstances. A cDNA library was constructed with an average fragment size of 500-1000 base pairs. The library was designed so that the inserts could be amplified by PCR in a highly uniform process using generic vector-derived primers, to provide DNA fragments that could be directly spotted onto microarrays. Clones from these

libraries were subjected to high throughput sequencing to confirm the diversity of the library

and identify novel sequences.

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Identification of the full-length sequences can be performed using in a number of different methods. For example, the gene can be isolated from a corresponding full-length eosinophil library or a library from a commercial source. Direct cloning from mRNA using a variety of techniques such as "5' race" is also possible.

Microarrays were generated using the library clones or the information derived from their sequence. The microarrays were used to generate differential mRNA expression data for eosinophils isolated from different sources or under the different conditions as described above (e.g. disease and normal or with and without treatment of IL-5) or for comparison of eosinophil mRNA with mRNA isolated from other cell types.

Variation was normalised to allow comparison of data from different microarrays by empirical selection of invariant genes followed by normalisation across this set. Although this approach was found to provide the most reliable and accurate data a variety of alternative normalisation methods could be envisaged by the skilled man, including global normalisation across the whole array, incorporation of a known mRNA or 'spike' as an internal standard in each sample, or normalisation to a housekeeping gene or genes (e.g. GAPDH, actin).

It is apparent that the polynucleotides or fragments thereof of the second aspect of the invention may be utilised in the above described methodology, for the identification of further polynucleotides and polypeptides which play a role in eosinophil mediated disease, such as inflammatory disease.

In a third aspect, the present invention relates to polynucleotide sequences that are capable of hybridising to any of the polynucleotide sequences which encode amino-acid sequences encoded by Seq ID Nos: 1-466 or to any of Seq ID Nos: 1-466 themselves, under stringent conditions, as defined above. In a preferred embodiment of the third aspect, there is provided polynucleotide sequences which are complimentary to the polynucleotide sequences which encode amino-acid sequences encoded by Seq ID Nos: 1-466, such as sequences which are complementary to any of Seq ID Nos: 1-466.

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Although the nucleotide sequences of the third aspect are capable of hybridising to the naturally occurring polynucleotide sequences under stringent conditions as described above, included

within the scope of the third aspect are polynucleotide sequences which hybridise to polynucleotide sequences having different codon usage, as a result of the degenracy of the genetic code.

The polynucleotide sequences according to the third aspect of the invention are useful in antisense technology, for example in the modulation and/or surpression of polynucleotide expression by interfering with the proper transcription or translation of the polynucleotide sequence. This modulation and/or surpression of polynucleotide expression may be useful in abolishing or alleviating disease symptoms associated with the polynuleotide sequences. In a preferred embodiment, the third aspect relates to a method of modulating or surpressing expression of a polynucleotide sequence which encodes an amino-acid sequence encoded by any of Seq ID Nos: 1-466 or fragments of those amino acid sequences, by administering a polynucleotide sequence, or fragment thereof, which hybridises under stringent conditions to the polynucleotide sequence being expressed.

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Such methods which suppress expression of the polynucleotide sequences may be used to elaborate on the functional properties of the polynucleotide sequences and their expression products. For example, cellular assays may be conducted in which key eosinophil responses are measured in response to normal and surpressed polynucleotide expression. The methods may also be used to abolish or alleviate the symptoms or cause of disease in a subject. In such a method, a polynucleotide sequence or fragment therof according to the third aspect of the invention may be administered to a subject. Two distinct 'antisense' methodologies are favoured. In one preferred method polynucleotides of approximately 20 bases complementary to the mRNA coding sequence are used to disable the gene of interest. In the other preferred 'antisense' methodology, the whole or a fragment of the gene sequence is inserted into an expression vector in an antisense orientation (3' to 5') under the control of a mammalian promoter and/or enhancer sequence.

For the first of the above methods, numerous techniques are available which assist in the design of suitable antisense oligonucleotides including, for example, the determination of loops in the mRNA structure using software based on thermodynamic stability calculations of the secondary and/or tertiary mRNA structures, RNAse H mapping of open sites using semi-random oligonucleotides and oligonucleotides designed to bind at defined intervals along the mRNA sequence. An electronic mapping procedures based on the mFold programme may be used to generate a short list of antisense oligonucleotides. The oligonucleotides may then tested in cellular assays to select potent and specific antisense oligonucleotides that suppress expression of

polynucleotide sequences, preferably by surpressing levels of the transcribed mRNA, prior to their use in functional assays or therapeutic methods described above.

Antisense oligonucleotides can be modified in a variety of ways, including the use of methyl phosphonate, methoxy-,ethoxy- or other base modifications and phosphorothioate to increased stability, cellular uptake, mRNA affinity and decreased non-specific protein or mRNA/DNA binding affinity, whilst maintaining their ability to induce RNAse H cleavage or block transcription/translation. In addition to identifying a potent and specific antisense oligonucleotide, the antisense oligonucleotide must be effectively delivered to the cell of interest. Preferably, the antisense oligonucleotide is produced by PCR techniques.

Using the second preferred 'antisense' methodology involves inserting the whole or a fragment of the polynucleotide sequence into an expression vector in an anitsense orientation (3' to 5') under the control of a promoter and/or enhancer sequence. Introduction of this sequence into the cell of interest and transcription of the antisense mRNA is expected to reduce the quantity of mRNA available for translation, thus reducing the level of polypeptide expressed by the polynucleotide

sequence. The antisense sequence can be introduced into a variety of different vectors (e.g. plasmid vectors, adenoviral and retroviral vectors) for delivery into cells prior to performing

functional cellular assays.

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Retroviral vectors are preferred as they have a number of advantages over the other delivery systems including ease of construction, high transduction and expression efficiencies, integration of the expression cassette into the host chromosome and the ability to deliver to both dividing and non-dividing cells). Retroviral vectors based on malony monkey leukaemia virus (MMLV) enable delivery to a variety of dividing human cells by virtue of being pseudotyped with different envelope proteins (e.g. VSV-G and amphotrophic MLV envelope). A commercial retroviral vector system comprising murine leukmia virus(MuLV) was also used. Replication deficient vectors based on lentiviruses such as human immunodeficiency virus (HIV), feline immunodeficiency virus (FIV) or equinr immunodeficiency virus (EIAV), if pseudotyped with appropriate envelope proteins, offer the potential of delivering to non-dividing or terminally differentiated cells, for example eosinophils.

In addition to the expression of antisense RNA, the retroviral vectors provide an ideal vehicle for the delivery of full length or fragments of the polynucleotide sequences in a sense orientation. Full length expression provides evidence for the role of the target, particularly relevant if it were found to be 'up' regulated in disease. Whilst expression of a fragment of the sequence could result in the production of a dominant negative protein or provide information regarding a possible splice variant of the gene.

For both antisense methodologies and the over expression studies, it is essential that mRNA levels of the target and control polynucleotide sequences are measured accurately to ensure specificity and validity. PCR based methods are preferred because of their sensitivity of detection particularly following mRNA antisense suppression. A variety of PCR based techniques are available including gel based quantitative or semi-quantitative methods and densitrometric measurement, in solution based methods using DNA intercolating fluorescent dyes or hybridisation of complementary labelled polynucleotides, the Taqman system from Perkin Elmer is preferred as this system offers good reproducibility, accuracy, real time quantitation and relatively high through put.

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In a preferred embodiment of the second or third aspects of the invention, the polynucleotide sequences may be ligated to a heterologous sequence to encode a fusion protein. For example, to screen peptide libraries for inhibitors, it may be useful to encode a chimeric protein that can be recognised by a commercially available antibody. A fusion protein may also be engineered to contain a cleavage site located between the sequence encoding the peptide of interest and the heterologous protein sequence, so that the peptide of interest may be cleaved and purified away from the heterologous moiety.

The polynucleotide sequences of the second and third aspects of the invention may be operably linked to any regulatory region, i.e., promoter and/or enhancer element known in the art, but these regulatory elements must be functional in the host cell selected for expression. The regulatory regions may comprise a promoter region for functional transcription in the host cell, and optionally a region situated 3' of the gene of interest, and which specifies a signal for termination of transcription and a polyadenylation site. A replication origin may also be included. Polynucleotide sequences of this embodiment may be referred to as expression cassettes. Promoters that may be used in the present invention include both constitutive promoters and regulated (inducible) promoters. The promoter may one which naturally controls the expression of the polynucleotide sequence, or where the polynucleotide sequence is in an antisense configuration, the promoter is one which naturally controls the expression of the sense configuration of the polynucleotide sequence. When the nucleic acid does not contain a promoter sequence, an appropriate promoter sequence may be inserted.

Promoters may be from a heterologous source. In particular, they may be promoter sequences of eukaryotic or viral genes. For example, a promoter sequence may be derived from the genome of the host cell which is to be infected. Likewise, promoter sequences may be derived from the genome of a virus, such as adenovirus (E1A and MLP), cytomegalovirus, or Rous Sarcoma Virus. In addition, the promoter may be modified by addition of activating or regulatory sequences, or sequences which confer a specific expression pattern, for example tissue-specific or predominant expression (enolase and GFAP promoters etc.). Such promoters would be known to a person skilled in the art.

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Suitable promoters useful for practice of this invention include ubiquitous promoters (e.g., HPRT, vimentin, actin, tubulin), intermediate filament promoters (e.g., desmin, neurofilaments, keratin, GFAP), therapeutic gene promoters (e.g., MDR type, CFTR, factor VIII), tissue-specific promoters (e.g., actin promoter in smooth muscle cells), promoters which are preferentially activated in dividing cells, promoters which respond to a stimulus (e.g., steroid hormone receptor, retinoic acid receptor), tetracycline-regulated transcriptional modulators, cytomegalovirus (CMV) immediate-early, retroviral LTR, metallothionein, SV-40, adenovirus E1a, and adenovirus major late (MLP) promoters. Tetracycline-regulated transcriptional modulators and CMV promoters are described in WO 96/01313, US 5,168,062 and 5,385,839, the contents of which are incorporated herein by reference. Further preferred promoters include, but are not limited to, the SV40 early promoter region (Benoist and Chambon, 1981, Nature 290:304-310), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto, et al., 1980, Cell 22:787-797), the herpes thymidine kinase promoter (Wagner et al., 1981, Proc. Natl. Acad. Sci. U.S.A. 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster et al., 1982, Nature 296:39-42); prokaryotic expression vectors such as the βlactamase promoter (Villa-Kamaroff, et al., 1978, Proc. Natl. Acad. Sci. U.S.A. 75:3727-3731), or the tac promoter (DeBoer, et al., 1983, Proc. Natl. Acad. Sci. U.S.A. 80:21-25); see also "Useful proteins from recombinant bacteria" in Scientific American, 1980, 242:74-94; promoter elements from yeast or other fungi such as the Gal 4 promoter, the ADC (alcohol dehydrogenase) promoter, PGK (phosphoglycerol kinase) promoter, alkaline phosphatase promoter; and the animal transcriptional control regions, which exhibit tissue specificity and have been utilized in transgenic animals: elastase I gene control region which is active in pancreatic acinar cells (Swift et al., 1984, Cell 38:639-646; Ornitz et al., 1986, Cold Spring Harbor Symp. Quant. Biol. 50:399-409; MacDonald, 1987, Hepatology 7:425-515); insulin gene control region which is active in pancreatic beta cells (Hanahan, 1985, Nature 315:115-122), immunoglobulin gene control region which is active in lymphoid cells (Grosschedl et al., 1984, Cell 38:647-658; Adames et al., 1985,

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Nature 318:533-538; Alexander et al., 1987, Mol. Cell. Biol. 7:1436-1444), mouse mammary tumour virus control region which is active in testicular, breast, lymphoid and mast cells (Leder et al., 1986, Cell 45:485-495), albumin gene control region which is active in liver (Pinkert et al., 1987, Genes and Devel. 1:268-276), alpha-fetoprotein gene control region which is active in liver (Krumlauf et al., 1985, Mol. Cell. Biol. 5:1639-1648; Hammer et al., 1987, Science 235:53-58), alpha 1-antitrypsin gene control region which is active in the liver (Kelsey et al., 1987, Genes and Devel. 1:161-171), beta-globin gene control region which is active in myeloid cells (Mogram et al., 1985, Nature 315:338-340; Kollias et al., 1986, Cell 46:89-94), myelin basic protein gene control region which is active in oligodendrocyte cells in the brain (Readhead et al., 1987, Cell 48:703-712), myosin light chain-2 gene control region which is active in skeletal muscle (Sani, 1985, Nature 314:283-286), and gonadotropic releasing hormone gene control region which is active in the hypothalamus (Mason et al., 1986, Science 234:1372-1378).

Additional regulatory regions may be identified using the polynucleotides of the present invention. The polynucleotide sequence may be extended using various methods known in the art to detect upstream sequences such as promoters and regulatory elements. One such method which may be employed is restriction-site PCR which uses universal primers to retrieve unknown sequence adjacent to a known locus (see, e.g., Sarkar, G. (1993) PCR Methods Applic. 2:318-322). In particular, genomic DNA is first amplified in the presence of a primer which is complementary to a linker sequence within the vector and a primer specific to a region of the nucleotide sequence. The amplified sequences are then subjected to a second round of PCR with the same linker primer and another specific primer internal to the first one. Products of each round of PCR are transcribed with an appropriate RNA polymerase and sequenced using reverse transcriptase.

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The polynucleotide sequences of the second and third aspects of the invention may also be operably linked to a 3' regulatory region, for example a 3' UTR sequence, or downstream promoter and/or enhancer sequences. Downstream 3' untranslated regions (3'UTR) have a well recognised role in mRNA stability (Nucleic Acids Symp Ser 1997;(36):29-32, Microbiol Rev 1995 Sep;59(3):423-50). The stability of an mRNA plays a major role in the determination of gene expression. The stability of an mRNA reflects its structure, as well as its interaction with transacting RNA-binding proteins. The processes that regulate mRNA stability can effect how cells grow, differentiate, and respond to their environment, and as such represent potential sites for therapeutic intervention. The polynucelotides of the present invention may be used to identify novel 3' UTR's, which may be useful in the isolation of further full length cDNA clones, which may have a role in inflammatory disease. This may be done using standard methodologies

including: electronic extension by comparison with DNA databases, PCR based strategies such as RACE, and screening of cDNA libraries. 3' UTR's also have utility as electronic probes and can be used as probes to measure corresponding gene specific mRNA levels in cells or tissues, using a number of techniques well known in the art for example: RT-PCR, In-situ hybridisation, Northern blotting, and microarray based techniques. This may be useful in diagnostic or prognostic assays, or functional assays. Finally, such 3' UTR's may be useful in the design of antisense oligonucleotides, which have a range of utilities as discussed above.

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Upstream or downstream regulatory regions of the polynucleotide sequences of the second aspect of the invention may be identified using inverse PCR, to amplify or extend sequences using divergent primers based on a known region. (See, e.g., Triglia, T. et al. (1988) Nucleic Acids Res. 16:8186.) The primers may be designed using commercially available software such as OLIGO 4.06 Primer Analysis software (National Biosciences Inc., Plymouth, MN) or another appropriate program to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the target sequence at temperatures of about 68°C to 72°C. The method uses several restriction enzymes to generate a suitable fragment in the known region of a gene. The fragment is then circularised by intramolecular ligation and used as a PCR template. Another method which may be used is capture PCR, which involves PCR amplification of DNA fragments adjacent to a known sequence in human and yeast artificial chromosome DNA (See, eg Lagerstrom, M. et al (1991) PCR Methods Applic. 1:111-119). In this method multiple restriction enzyme digestions and ligations may be used to place an engineered double-stranded sequence into an unknown fragment of the DNA molecule before performing PCR. Other methods which may be used to retrieve unknown sequences are well known in the art (see eg Parker, J.D. et al (1991) Nucleic Acids Res. 19:3055-3060). Additionally, one may use PCR, nested primers and PromoterFinder™ libraries to walk genomic DNA (Clontech, Palo Alto,CA). This process avoids the need to screen libraries and is useful in finding intron/exon junctions.

When screening for full-length cDNAs, it is preferable to use libraries that have been size-selected to include larger cDNAs. Also, random-primed libraries are preferable in that they will include more sequences which contain the 5' regions of genes. Use of a randomly primed library may be especially preferable for situations in which an oligo d(T) library does not yield a full-length cDNA. Genomic libraries may be useful for extension of sequence into 5' non-transcribed regulatory regions.

Capillary electrophoresis systems which are commercially available may be used to analyse the size or confirm the nucleotide sequence of sequencing or PCR products. In particular, the

capillary sequencing may employ flowable polymers for electrophoretic separation, four different fluorescent dyes (one for each nucleotide) which are laser activated, and a charge coupled device camera for detection of the emitted wavelengths. Output/light intensity may be converted to electrical signal using appropriate software (eg Genotyper<sup>TM</sup> and Sequence Navigator<sup>TM</sup>, Perkin Elmer) and the entire process from loading of samples to computer analysis and electronic data display may be computer controlled. Capillary electrophoresis is especially preferable for sequencing small pieces of DNA which might be present in limited amounts in a particular sample.

In a further preferred embodiment of the second and third aspects of the present invention, the polynucleotide sequences may be engineered using methods generally known in the art in order to alter the sequences for a variety of reasons including, but not limited to, alterations which modify the cloning, processing, and/or expression of the gene product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. For example, site-directed mutagenesis may be used to insert new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, introduce mutations, and so forth. Further, as will be understood by those of skill in the art, it may be advantageous to produce nucleotide sequences possessing non-naturally occurring codons. For example codons preferred by a particular prokaryotic or eukaryotic host can be selected to increase the rate of protein expression or to produce RNA transcript having desirable properties such as a half-life which is longer than that of a transcript generated from the naturally occurring sequence.

In another preferred embodiment of the second and third aspects of the present invention, there is provided an expression vector comprising one or more polynucleotide sequences according to the second or third aspects of the invention. As will be apparent to a person skilled in the art, the choice of expression vector may depend upon the characteristics of the polynucleotide sequence to be expressed and the expression systmen used. Useful expression vectors, for example, may consist of segments of chromosomal, non-chromosomal and synthetic DNA sequences. Suitable vectors include derivatives of SV40 and known bacterial plasmids, e.g., E. coli plasmids col El, pCR1, pBR322, pMal-C2, pET, pGEX (Smith et al., 1988, Gene 67:31-40), pMB9 and their derivatives, plasmids such as RP4; phage DNAS, e.g., the numerous derivatives of phage l, e.g., NM989, and other phage DNA, e.g., M13 and filamentous single stranded phage DNA; yeast plasmids such as the 2m plasmid or derivatives thereof; vectors useful in eukaryotic cells, such as vectors useful in insect or mammalian cells; vectors derived from combinations of plasmids and phage DNAs, such as plasmids that have been modified to employ phage DNA or other expression control sequences; and the like.

For example, in a baculovirus expression systems, both non-fusion transfer vectors, such as but not limited to pVL941 (BamH1 cloning site; Summers), pVL1393 (BamH1, SmaI, XbaI, EcoR1, NofI, XmaIII, BgIII, and PsfI cloning site; Invitrogen), pVL1392 (BgIII, PsfI, NofI, XmaIII, EcoRI, XbaI, SmaI, and BamH1 cloning site; Summers and Invitrogen), and pBlueBacIII (BamH1, BgIII, PsfI, NcoI, and HindIII cloning site, with blue/white recombinant screening possible; Invitrogen), and fusion transfer vectors, such as but not limited to pAc700 (BamH1 and KpnI cloning site, in which the BamH1 recognition site begins with the initiation codon; Summers), pAc701 and pAc702 (same as pAc700, with different reading frames), pAc360 (BamH1 cloning site 36 base pairs downstream of a polyhedrin initiation codon; Invitrogen(195)), and pBlueBacHisA, B, C (three different reading frames, with BamH1, BgIII, PsfI, NcoI, and HindIII cloning site, an N-terminal peptide for ProBond purification, and blue/white recombinant screening of plaques; Invitrogen (220)) can be used.

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Mammalian expression vectors contemplated for use in the invention include vectors with 15 inducible promoters, such as the dihydrofolate reductase (DHFR) promoter, e.g., any expression vector with a DHFR expression vector, or a DHFR/methotrexate co-amplification vector, such as pED (PstI, Sall, SbaI, SmaI, and EcoRI cloning site, with the vector expressing both the cloned gene and DHFR; see Kaufman, Current Protocols in Molecular Biology, 16.12 (1991). Alternatively, a glutamine synthetase/methionine sulfoximine co-amplification vector, such as 20 pEE14 (HindIII, XbaI, SmaI, SbaI, EcoRI, and BcII cloning site, in which the vector expresses glutamine synthase and the cloned gene; Celltech). In another embodiment, a vector that directs episomal expression under control of Epstein Barr Virus (EBV) can be used, such as pREP4 (BamH1, Sfil, XhoI, Notl, NheI, HindIII, NheI, PvuII, and KpnI cloning site, constitutive Rous Sarcoma Virus Long Terminal Repeat (RSV-LTR) promoter, hygromycin selectable marker; 25 Invitrogen), pCEP4 (BamH1, Sfil, Xhol, Notl, Nhel, HindIII, Nhel, PvuII, and KpnI cloning site, constitutive human cytomegalovirus (hCMV) immediate early gene, hygromycin selectable marker; Invitrogen), pMEP4 (KpnI, PvuI, NheI, HindIII, NotI, XhoI, SfiI, BamH1 cloning site, inducible methallothionein IIa gene promoter, hygromycin selectable marker: Invitrogen), pREP8 (BamH1, XhoI, NotI, HindIII, NheI, and KpnI cloning site, RSV-LTR promoter, histidinol 30 selectable marker; Invitrogen), pREP9 (KpnI, NheI, HindIII, NotI, XhoI, SfiI, and BamHI cloning site, RSV-LTR promoter, G418 selectable marker; Invitrogen), and pEBVHis (RSV-LTR promoter, hygromycin selectable marker, N-terminal peptide purifiable via ProBond resin and cleaved by enterokinase; Invitrogen). Selectable mammalian expression vectors for use in the invention include pRc/CMV (HindIII, BstXI, NotI, ShaI, and ApaI cloning site, G418 selection; 35 Invitrogen), pRc/RSV (HindIII, SpeI, BstXI, NotI, XbaI cloning site, G418 selection; Invitrogen),

and others. Vaccinia virus mammalian expression vectors (see, Kaufman, 1991, supra) for use according to the invention include but are not limited to pSC11 (SmaI cloning site, TK- and  $\beta$ -gal selection), pMJ601 (SaII, SmaI, AfII, NarI, BspMII, BamHI, ApaI, NheI, SacII, KpnI, and HindIII cloning site; TK- and  $\beta$ -gal selection), and pTKgptF1S (EcoRI, PstI, SaII, AccI, HindII, SbaI, BamHI, and Hpa cloning site, TK or XPRT selection).

In another preferred embodiment, there are provided host cells comprising the polypeptide or polynucleotide sequences according to the first, second or third aspects of the invention. Preferably, a host cell is provided as an expression system, and thus may comprise a polynucleotide sequence or fragment thereof according to the second or third aspects of the invention. More preferably, the host cell will comprise an expression vector, such as described above, which comprises the polynucleotide sequence or fragment thereof. Suitable host cell strains or cell-free expression systems will be known to persons skilled in the art.

A host cell strain may be chosen which modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Different host cells have characteristic and specific mechanisms for the translational and post-translational processing and modification of proteins. Appropriate cell lines or host systems can be chosen to ensure the desired modification and processing of the foreign protein expressed. Expression in yeast can produce a biologically active product. Expression in eukaryotic cells can increase the likelihood of "native" folding. Moreover, expression in mammalian cells can provide a tool for reconstituting, or constituting, polypeptide activity. Furthermore, different vector/host expression systems may affect processing reactions, such as proteolytic cleavages, to a different extent.

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In a fourth aspect, the present invention relates to the production of the polynucleotide or polypeptide sequences, or fragments or variants thereof, according to the first, second or third aspects of the invention. The production of a polynucleotide or polypeptide sequence may comprise either recombinant or synthetic techniques. Where the method comprises production of the polypeptide or polynucleotide sequence by synthetic chemistry, preferably the entire polypeptide or or polynucleotide sequence, or desired fragment thereof is made using synthetic chemistry. Where a polynucleotide is produced, the synthetic sequence may be inserted into any expression vectors, such as those described above, and expressed in a expression system using reagents that are well known in the art. Moreover synthetic chemistry may be used to introduce modifications and/or mutations into an oligonucleotide sequence or a fragment thereof.

The polynucleotide sequences may be synthesised, in whole or in part, using chemical methods well known in the art. (See, e.g., Caruthers, M.H. et al. (1980) Nucl. Acids Res. Symp. Ser. 215-223, and Horn, T. et al. (1980) Nuc.l. Acids Res. Symp. Ser. 225-232). Alternatively, the polypeptide may be produced using chemical methods to synthesize the amino acid sequence of any one or more of Figure 1 to 357, or a fragment thereof. For example, peptide synthesis can be performed using various solid-phase techniques. (See, e.g., Roberge, J.Y. et al. (1995) Science 269:202-204). Automated synthesis may be achieved using the ABI 43 IA Peptide Synthesizer (Perkin Elmer). Additionally, the amino acid sequence, or any part thereof, may be altered during direct synthesis and/or combined with sequences from other proteins, or any part thereof, to produce a variant polypeptide. The polypeptide may be substantially purified by preparative high performance liquid analysis or by sequencing. (See for example: Creighton, T. (1983) Proteins. Structures and Molecular Properties, WH Freeman and Co., New York).

In a preferred embodiment of the fourth apsect of the invention, there is provided a method for directing the expression of the polypeptide sequences or fragments thereof of the first aspect of the invention in appropriate host cells. Preferably, this method employs recombinant DNA technology to result in expression of polypeptides according to the first aspect of the invention. The method of producing a polypeptide according to the first aspect of the invention, comprises:

a) transforming a host cell with a polynucleotide sequence according to the second or third aspects of the invention;

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- b) culturing the host cell under conditions suitable for expression of the polypeptide; and
- c) recovering the polypeptide from the host cell culture.

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The polynucleotide sequence introduced into the host cell may be in the form of an expression vector, having the necessary regulatory sequences such as promoters and/or enhancers, and transcriptional and translational signals, as discussed above. The polynucleotide sequence may be flanked by its' native upstream and/or downstream regulatory regions. Potential host-vector systems include but are not limited to mammalian cell systems infected with virus (e.g., vaccinia virus, adenovirus, etc.); insect cell systems infected with virus (e.g., baculovirus); microorganisms such as yeast containing yeast vectors; or bacteria transformed with bacteriophage, DNA, plasmid DNA, or cosmid DNA. The expression elements of vectors vary in their strengths and specificities. Depending on the host-vector system utilised, any one of a number of suitable transcription and translation elements may be used. Yeast expression systems can also be used to express polypeptides of the present invention. For example, the non-fusion pYES2 vector (XbaI, SphI, ShoI, NotI, GstXI, EcoRI, BstXI, BamH1, SacI, Kpn1, and HindIII cloning sit; Invitrogen) or the fusion pYESHisA, B, C (XbaI, SphI, ShoI, NotI, BstXI, EcoRI,

BamH1, SacI, KpnI, and HindIII cloning site, N-terminal peptide purified with ProBond resin and cleaved with enterokinase; Invitrogen), to mention just two, can be employed according to the invention.

Alternatively, the polynucelotide sequence of the invention or fragment thereof, may be expressed chromosomally, after integration of the coding sequence by recombination. In this regard, any of a number of amplification systems may be used to achieve high levels of stable gene expression (See Sambrook et al., 1989, supra). Any method for the insertion of DNA fragments into a cloning vector may be used to construct expression vectors containing a gene consisting of appropriate transcriptional/translational control signals and the protein coding sequences. These methods may include in vitro recombinant DNA and synthetic techniques and in vivo recombination (genetic recombination). Such methods will be known to a person skilled in the art.

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Vectors are introduced into the desired host cells by methods known in the art, e.g., transfection, electroporation, microinjection, transduction, cell fusion, DEAE dextran, calcium phosphate precipitation, lipofection (lysosome fusion), use of a gene gun, or a DNA vector transporter (see, e.g., Wu et al., 1992, J. Biol. Chem. 267:963-967; Wu and Wu, 1988, J. Biol. Chem. 263:14621-14624; Hartmut et al., Canadian Patent Application No. 2,012,311, filed March 15, 1990).

Expression vectors containing a polynucleotide of the invention can be identified by five general approaches: (a) PCR amplification of the desired plasmid DNA or specific mRNA, (b) nucleic acid hybridization, (c) presence or absence of selection marker gene functions, (d) analysis with appropriate restriction endonucleases, and (e) expression of inserted sequences. In the first approach, the nucleic acids can be amplified by PCR to provide for detection of the amplified product. In the second approach, the presence of a foreign gene inserted in an expression vector can be detected by nucleic acid hybridization using probes comprising sequences that are homologous to an inserted marker gene. In the third approach, the recombinant vector/host system can be identified and selected based upon the presence or absence of certain "selection marker" gene functions (e.g., β-galactosidase activity, thymidine kinase activity, resistance to antibiotics, transformation phenotype, occlusion body formation in baculovirus, etc.) caused by the insertion of foreign genes in the vector. In another example, if a polynucleotide sequence of the invention is inserted within a "selection marker" gene sequence of the vector. Recombinants containing an insert can then be identified by the absence of the gene function. In the fourth approach, recombinant expression vectors are identified by digestion with appropriate

restriction enzymes. In the fifth approach, recombinant expression vectors can be identified by

assaying for the activity, biochemical, or immunological characteristics of the gene product expressed by the recombinant, provided that the expressed protein assumes a functionally active conformation.

Once a particular recombinant DNA molecule is identified and isolated, several methods known in the art may be used to propagate it. Once a suitable host system and growth conditions are established, recombinant expression vectors can be propagated and prepared in quantity.

Soluble forms of the protein can be obtained by collecting culture fluid, or solubilising inclusion bodies, e.g., by treatment with detergent, and if desired sonication or other mechanical processes, as described above. The solubilised or soluble protein can be isolated using various techniques, such as polyacrylamide gel electrophoresis (PAGE), isoelectric focusing, 2-dimensional gel electrophoresis, chromatography (e.g., ion exchange, affinity, immunoaffinity, and sizing column chromatography), centrifugation, differential solubility, immunoprecipitation, or by any other standard technique for the purification of proteins.

In accordance with the present invention there may be employed conventional molecular biology, microbiology, and recombinant DNA techniques within the skill of the art. Such techniques are explained fully in the literature. See, e.g., Sambrook, Fritsch & Maniatis, Molecular Cloning: A Laboratory Manual, Second Edition (1989) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York; DNA Cloning: A Practical Approach, Volumes I and II (D.N. Glover ed. 1985); Oligonucleotide Synthesis (M.J. Gait ed. 1984); Nucleic Acid Hybridization [B.D. Hames & S.J. Higgins eds. (1985)]; Transcription And Translation [B.D. Hames & S.J. Higgins, eds. (1984)]; Animal Cell Culture [R.I. Freshney, ed. (1986)]; Immobilized Cells And Enzymes [IRL Press, (1986)]; B. Perbal, A Practical Guide To Molecular Cloning (1984); F.M. Ausubel et al. (eds.), Current Protocols in Molecular Biology, John Wiley & Sons, Inc. (1994).

Methods for DNA sequencing are well known and generally available in the art and may be used to practice any of the embodiments of the invention. The methods may employ such enzymes as the Klenow fragment of DNA polymerase I, TM (US Biochemical Corp., Cleveland, OH), Taq polymerase (Perkin Elmer), thermostable T7 polymerase (Amersham, Chicago, IL), or combinations of polymerases and proof reading exonucleases such as those found in the ELONGASE Amplification System (GIIBCO/BRL, Gaithersburg, MD). Preferably, the process is automated with machines.

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In a fifth aspect of the invention, there is provided an antibody or fragment thereof which binds to a polypeptide according to the first aspect of the invention. Also provided are methods for production of such antibodies or fragments thereof, using the polypeptides, or fragments thereof, of the first aspect as antigens. Fusion proteins as described above may also be used for the generation of antibodies.

A molecule is "antigenic" when it is capable of specifically interacting with an antigen recognition molecule of the immune system, such as an immunoglobulin (antibody) or T cell antigen receptor. An antigenic polypeptide contains at least about 5, and preferably at least about 10, amino acids. An antigenic portion of a molecule can be that portion that is immunodominant for antibody or T cell receptor recognition, or it can be a portion used to generate an antibody to the molecule by conjugating the antigenic portion to a carrier molecule for immunisation. A molecule that is antigenic need not be itself immunogenic, i.e., capable of eliciting an immune response without a carrier.

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The antibodies of the fifth aspect include but are not limited to polyclonal, monoclonal, chimeric, single chain, Fab fragments, and an Fab expression library. The antibodies of the invention may be cross reactive, ie they may recognise different antigenic species. Polyclonal antibodies have greater likelihood of cross reactivity. Alternatively, an antibody of the invention may be specific for a single polypeptide. Preferably, such an antibody is specific for the polypeptides of the invention.

Various procedures known in the art may be used for the production of polyclonal antibodies. For the production of antibody, various host animals can be immunised by injection with a polypeptide of the invention, or a derivative (e.g., fragment or fusion protein) thereof, including but not limited to rabbits, mice, rats, sheep, goats, etc. In one embodiment, a polypeptide or fragment thereof can be conjugated to an immunogenic carrier, e.g., bovine serum albumin (BSA) or keyhole limpet hemocyanin (KLH). Various adjuvants may be used to increase the immunological response, depending on the host species, including but not limited to Freund's (complete and incomplete), mineral gels such as aluminium hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanins, dinitrophenol. Among adjuvants used in humans, BCG (bacilli Calmette-Guerin) and 5 Colynebacte arvum are especially preferable. It is preferred that the polypeptides, or fragments used to induce antibodies have an amino acid sequence consisting of at least about 5 amino acids, and, more preferably, of at least about 10 amino acids. It is also preferable that these polypeptides, or fragments are identical to a portion of the amino acid sequence of the

WO 02/10198 PCT/GB01/03390

natural protein. Short stretches of amino acids may be fused with those of another protein, such as KLH and antibodies to the chimeric molecule may be produced.

Monoclonal antibodies directed towards a polypeptide of the invention, or fragment, or analog, or derivative thereof may be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to the hybridoma technique originally developed by Kohler and Milstein [Nature 256:495-497 (1975)], as well as the trioma technique, the human B-cell hybridoma technique [Kozbor et al., Immunology Today 4:72 1983); Cote et al., Proc. Natl. Acad. Sci. U.S.A. 80:2026-2030 (1983)], and the EBV-hybridoma technique to produce human monoclonal antibodies [Cole et al., in Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc., pp. 77-96 (1985)].

In another embodiment of the fifth aspect, monoclonal antibodies can be produced in germ-free animals [International Patent Publication No. WO 89/12690, published 28 December 1989].

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Techniques developed for the production of "chimeric antibodies" such as [Morrison et al., J. Bacteriol. 159:870 (1984); Neuberger et al., Nature 312:604-608 (1984); Takeda et al., Nature 314:452-454 (1985)] by splicing the genes from a mouse antibody molecule specific for a polypeptide of the invention together with genes from a human antibody molecule of appropriate biological activity can also be used; and such antibodies are within the scope of this invention. Such human or humanized chimeric antibodies are preferred for use in therapy of human diseases or disorders (described infra), since the human or humanized antibodies are much less likely than xenogenic antibodies to induce an immune response, in particular an allergic response, themselves.

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According to the invention, techniques described for the production of single chain Fv (scFv) antibodies [U.S. Patent Nos. 5,476,786 and 5,132,405 to Huston; U.S. Patent 4,946,778] can be adapted to produce polypeptide-specific single chain antibodies.

An additional embodiment of the invention utilises the techniques described for the construction of Fab expression libraries Huse et al., Science 246:1275-1281 (1989) to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity for a polypeptide of the invention, or its derivatives, or analogs. Antibody fragments which contain the idiotype of the antibody molecule can be generated by known techniques. For example, such fragments include but are not limited to: the F(ab')<sub>2</sub> fragment which can be produced by pepsin digestion of the antibody molecule; the Fab' fragments which can be generated by reducing the disulfide bridges

of the F(ab')<sub>2</sub> fragment, and the Fab fragments which can be generated by treating the antibody molecule with papain and a reducing agent.

In the production of antibodies, screening for the desired antibody can be accomplished by techniques known in the art, e.g., radioimmunoassay, ELISA (enzyme-linked immunosorbent assay), "sandwich" immunoassays, immunoradiometric assays, gel diffusion precipitin reactions, immunodiffusion assays, in situ immunoassays (using colloidal gold, enzyme or radioisotope labels, for example), western blots, precipitation reactions, agglutination assays (e.g., gel agglutination assays, hemagglutination assays), complement fixation assays, immunofluorescence assays, protein A assays, and immunoelectrophoresis assays, etc. In one embodiment, antibody binding is detected by detecting a label on the primary antibody. In another embodiment, the primary antibody is detected by detecting binding of a secondary antibody or reagent to the primary antibody. In a further embodiment, the secondary antibody is labelled. Many means are known in the art for detecting binding in an immunoassay and are within the scope of the present invention. For example, to select antibodies which recognise a specific epitope of a polypeptide of the present invention, one may assay generated hybridomas for a product which binds to an polypeptide fragment containing such epitope. For selection of an antibody specific to a polypeptide from a particular species of animal, one can select on the basis of positive binding with polypeptide expressed by or isolated from cells of that species of animal.

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The foregoing antibodies can be used in methods known in the art relating to the localisation and activity of the polypeptides of the present invention, e.g., for Western blotting, imaging polypeptide in situ, measuring levels thereof in appropriate physiological samples, etc. using any of the detection techniques mentioned above or known in the art.

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In a specific embodiment, antibodies that agonize or antagonize the activity of a polypeptide can be generated. Such antibodies can be tested using the assays described *infra* for identifying ligands. In particular, such antibodies can be scFv antibodies expressed intracellularly.

Histological analysis using these antibodies of the present invention can provide information on protein tissue distribution (disease and normal tissue), localisation of the protein within cells and the extracellular environment. The antibodies of the present invention can also provide functional information by acting as agonists or antagonists of the protein encoded by the novel gene in question both in vitro and in vivo.

In a sixth aspect, the present invention relates to a method of screening for agents which modify the expression and/or activity of one or more of the polynucleotides or polypeptides of the present invention, or derivatives thereof, the method comprising the steps of:

- 5 a) exposing one or more of the polynucleotides or polypeptides or derivatives thereof to at least one agent to be screened; and
  - b) detecting and/or measuring interaction and/or binding between the polynucleotide or polypeptide or derivatives thereof and the agent.
- Preferably, the polynucleotides are those of the second or third aspect of the invention, more preferably the polynucleotide sequences of any of Seq ID Nos: 1-466, or fragments thereof. The polypeptide sequences are preferably those encoded by any of Seq ID Nos: 1-466, or fragments thereof.
- The polypeptides or polynucleotides of the present invention, or derivatives thereof including catalytic or immunogenic fragments, or oligopeptides can be used for screening libraries of compounds in any of a variety of drug screening techniques. The polypeptides or polynucleotides of the present invention, or derivatives thereof employed in such screening may be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly.

  The formation of binding complexes between the polypeptides or polynucleotides of the present invention, or derivatives thereof and the agent being tested may be measured.

Another technique for drug screening provides for high throughput screening of compounds having suitable binding affinity to a polypeptide of interest. (See, e.g., Geysen, et al. (1984) PCT application W084103564). In this method, large numbers of different small test compounds are synthesised on a solid substrate, such as plastic pins or some other surface. The test compounds are reacted with a polypeptide of the present invention, or one or more fragments thereof, and washed. Bound polypeptide is then detected by methods well known in the art. Purified polypeptide can also be coated directly onto plates for use in the aforementioned drug screening techniques. Alternatively, non-neutralising antibodies can be used to capture the peptide and immobilise it on a solid support.

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Identification and isolation of a polynucleotide encoding a polypeptide of the invention provides for expression of polypeptides in quantities greater than can be isolated from natural sources, or in indicator cells that are specially engineered to indicate the activity of a polypeptide expressed after transfection or transformation of the cells. Accordingly, in addition to rational design of agonists and antagonists based on the structure of a polypeptide, the present invention

contemplates an alternative method for identifying specific ligands of polypeptides of the invention using various screening assays known in the art.

Any screening technique known in the art can be used to screen for agents which either agonise or antagonise the polypeptides of the present invention. For example, a suitable cell line expressing a polypeptide of the invention, can be transfected with a nucleic acid encoding a marker gene, such as  $\beta$ -galactosidase. Cells are then exposed to a test solution comprising a putative agonist or antagonist, and then stained for  $\beta$ -galactosidase activity. The presence of more  $\beta$ -gal positive cells relative to control cells not exposed to the test solution is an indication of the presence of an agonist of the polypeptide in the test solution. Conversely, the presence of less  $\beta$ -gal positive cells relative to control cells not exposed to the test solution is an indication of the presence of an antagonist of the polypeptide in the test solution.

The present invention contemplates screens for small molecule ligands or ligand analogs and mimics, as well as screens for natural ligands that bind to and agonise or antagonise the polypeptides or polynucleotides of the present invention *in vivo*.

Knowledge of the primary sequence of a polynucleotide or polypeptide of the invention, and the similarity of that sequence with sequences of known function, can provide an indication of potential inhibitors or antagonists of a protein or polynucleotde. Identification and screening of antagonists is further facilitated by determining structural features of the polynucleotide or polypeptide, e.g., using X-ray crystallography, neutron diffraction, nuclear magnetic resonance spectrometry, and other techniques for structure determination. These techniques provide for the rational design or identification of agonists and antagonists.

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Another approach uses recombinant bacteriophage to produce large libraries. Using the "phage method" [Scott and Smith, 1990, Science 249:386-390 (1990); Cwirla, et al., Proc. Natl. Acad. Sci., 87:6378-6382 (1990); Devlin et al., Science, 249:404-406 (1990)], very large libraries can be constructed (10<sup>6</sup>-10<sup>8</sup> chemical entities). A second approach uses primarily chemical methods, of which the Geysen method [Geysen et al., Molecular Immunology 23:709-715 (1986); Geysen et al. J. Immunologic Method 102:259-274 (1987)] and the method of Fodor et al. [Science 251:767-773 (1991)] are examples. Furka et al. [14th International Congress of Biochemistry, Volume 5, Abstract FR:013 (1988); Furka, Int. J. Peptide Protein Res. 37:487-493 (1991)], Houghton [U.S. Patent No. 4,631,211, issued December 1986] and Rutter et al. [U.S. Patent No. 5,010,175, issued April 23, 1991] describe methods to produce a mixture of peptides that can be tested as agonists or antagonists.

In another embodiment, synthetic libraries [Needels et al., *Proc. Natl. Acad. Sci. USA* 90:10700-4 (1993); Ohlmeyer et al., *Proc. Natl. Acad. Sci. USA* 90:10922-10926 (1993); Lam et al., International Patent Publication No. WO 92/00252; Kocis et al., International Patent Publication No. WO 9428028, each of which is incorporated herein by reference in its entirety], and the like can be used to screen for ligands according to the present invention.

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The screening can be performed with recombinant cells that express a polypetide of the invention, or alternatively, using purified protein, e.g., produced recombinantly, as described above. For example, labelled, soluble peptides can be used to screen libraries, as described in the foregoing references.

In an embodiment, a polypeptide or polynucleotide or derivative thereof may be directly labelled. In another aspect of the invention a labelled secondary reagent may be used to detect binding of the polynucleotide or polypeptide or derivative thereof to an agent of interest, e.g., a molecule attached to a solid phase support. Binding may be detected by in situ formation of a chromophore by an enzyme label. Suitable enzymes include, but are not limited to, alkaline phosphatase and horseradish peroxidase. In a further embodiment, a two colour assay, using two chromogenic substrates with two enzyme labels on different acceptor molecules of interest, may be used. Cross-reactive and singly-reactive ligands may be identified with a two-colour assay.

Other labels for use in the invention include coloured latex beads, magnetic beads, fluorescent labels (e.g., fluorescene isothiocyanate (FITC), phycoerythrin (PE), Texas red (TR), rhodamine, free or chelated lanthanide series salts, especially Eu<sup>3+</sup>, to name a few fluorophores), chemiluminescent molecules, radio-isotopes, or magnetic resonance imaging labels. Two colour assays may be performed with two or more coloured latex beads, or fluorophores that emit at different wavelengths. Labelled moieties may be detected visually or by mechanical/optical means. Mechanical/optical means include fluorescence activated sorting, *i.e.*, analogous to FACS, and micromanipulator removal means.

In another embodiment, one may use competitive drug screening assays in which neutralising antibodies capable of binding the polypeptide specifically compete with a test compound for binding sites. In this manner, antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with a polypeptide of the present invention.

In a related aspect, the present invention relates to agents identified using the above screening method of the sixth aspect.

In a seventh aspect, the present invention also relates to pharmaceutical compositions. In one embodiment a polypeptide, polynucleotide, fragment thereof, antisense polynucleotide sequence, antibody or agent of the present invention, with or without a pharmaceutically acceptable carrier or vehicle may be administered to a subject for use in the diagnosis, prevention or treatment of disease, such as eosinophil mediated inflammatory disease. Such a disease may include, but is not limited to, asthma, emphysemia, COPD, bronchitis, allergic disorders such as atopic dermatitis and NERDS (nodules eosinophilia,rheumatism, dermatitis and swelling); vasculitic granulomatous diseases including polyarteritis, Wegeners granulomatosis; some autoimmune diseases; interstitial and other pulmonary diseases including eosinophilic pneumonia, sarcoiditis and idiopathic pulmonary fibrosis; and neoplastic and myoploriferative diseases including hypereosinophilic syndrome, T cell lymphoma and hodgkins disease.

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In a preferred embodiment, the pharmaceutical composition may comprise an antagonist of the polypeptides of the present invention for administration to a subject to treat or prevent an eosinophil mediated disorder. Such a disorder may include inflammatory disorders of any type, and includes but is not limited to, asthma, emphysemia, COPD, bronchitis, allergic disorders such as atopic dermatitis and NERDS (nodules eosinophilia,rheumatism, dermatitis and swelling); vasculitic granulomatous diseases including polyarteritis, Wegeners granulomatosis; some auto-immune diseases; interstitial and other pulmonary diseases including eosinophilic pneumonia, sarcoiditis and idiopathic pulmonary fibrosis; and neoplastic and myoploriferative diseases including hypereosinophilic syndrome, T cell lymphoma and hodgkins disease.

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In another embodiment, the pharmaceutical composition may comprise an antibody which specifically binds a polypeptide of the present invention, for use directly as an antagonist as described above, or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical agent to cells or tissue which express the polypeptide.

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In an additional embodiment, the pharmaceutical composition may comprise the complement of a polynucleotide of the second aspect, for administration to a subject to treat or prevent an inflammatory disease including, but not limited to, those described above. Preferably, a polynucleotide sequence according to the third aspect of the invention will be used. More preferably, the polynucleotide sequence will be in the form of an expression vector, as described above.

In an additional embodiment, the pharmaceutical composition may comprise the polynucleotide or polypeptide sequences, or fragments thereof, of the first and second aspects of the invention for use in treating or preventing an inflammatory disease, preferably an eosinphil mediated

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In further embodiments, any of the polypeptides, antagonists, antibodies, agonists, complementary sequences, or vectors of the invention may be administered in combination with other appropriate therapeutic agents. Selection of the appropriate agents for use in combination therapy may be made by one of ordinary skill in the art, according to conventional pharmaceutical principles. The combination of therapeutic agents may act synergistically to effect the treatment or prevention of the various disorders described above. Using this approach, one may be able to achieve therapeutic efficacy with lower dosages of each agent, thus reducing the potential for adverse side effects.

An antagonist of a polypeptide of the present invention may be produced using methods which are generally known in the art. In particular, purified polypeptide may be used to produce antibodies or to screen libraries of pharmaceutical agents to identify those which specifically bind to the polypeptide. Antibodies to a polypeptide of the invention may also be generated using methods that are well known in the art examples of which are described *supra*. Such antibodies may include, but are not limited to, polyclonal, monoclonal, chimeric, and single chain antibodies, Fab fragments, and fragments produced by a Fab expression library. Neutralising

antibodies (i.e., those which inhibit dimer formation) are especially preferred for therapeutic

In an eighth aspect of the invention, there is provided a method of prevention, or treatment of an

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inflammatory disease, in particular eosinphil mediated disease, comprising administration to a subject a polynucleotide or polypeptide or fragment thereof, or derivatives including complements, antibodies or agents. In one embodiment, a complement of a polynucleotide may be used in diagnosis, prevention or treatment of disease, for example in situations in which it would be desirable to block the transcription of the mRNA. In particular, cells may be transformed with sequences complementary to the polynucleotide of the present invention. Thus, complementary molecules or fragments may be used to modulate polypeptide activity, or to achieve regulation of gene function. Such technology is now well known in the art, and sense

the coding or control regions of sequences. Preferably, polynucleotide sequences according to the third aspect of the invention will be employed.

or antisense oligonucleotides or larger fragments can be designed from various locations along

In an embodiment of this aspect, it is envisaged that the polynucleotide sequences of the second aspect of the invention may be used in the treatment or prevention of an inflammatory disease, in particular, and eosinpohil mediated disease. For example, a polynucleotide sequence according to the second aspect may be administered to a subject by any method described below where it is found that disease or symptoms thereof are the result of a deficiency in a particular polynucleotide or polypeptide sequence. In an embodiment, the method may comprise direct administration of the polypeptide sequences according to the first aspect.

Expression vectors derived from retroviruses, adenoviruses, or herpes or vaccinia viruses, or from various bacterial plasmids, may be used for delivery of nucleotide sequences to the targeted organ, tissue, or cell population. Methods which are well known to those skilled in the art can be used to construct vectors which will express nucleic acid sequences complementary to the polynucleotides of the present invention (See, e.g., Sambrook, supra; and Ausubel, supra.)

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Genes can be turned off by transforming a cell or tissue with expression vectors which express high levels of a polynucleotide, or a fragment thereof. Such constructs may be used to introduce untranslatable sense or antisense sequences into a cell. Even in the absence of integration into the DNA, such vectors may continue to transcribe RNA molecules until they are disabled by endogenous nucleases. Transient expression may last for a month or more with a non-replicating vector, and may last even longer if appropriate replication elements are part of the vector system.

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As mentioned above, modifications of gene expression can be obtained by designing complementary sequences or antisense molecules (DNA, RNA, or PNA) to the control, 5', or regulatory regions of the polynucleotides of the present invention. Oligonucleotides derived from the transcription initiation site, e.g., between about positions -10 and +10 from the start site, are preferred. Similarly, inhibition can be achieved using triple helix base-pairing methodology. Triple helix pairing is useful because it causes inhibition of the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or regulatory molecules. Recent therapeutic advances using triplex DNA have been described in the literature. (See, e.g., Gee, J.E. et al. (1994) in Huber, B.E. and B.1. Carr, Molecular and Immunologic A1212roaches, Futura Publishing Co., Mt. Kisco, NY, pp. 163-177.) A complementary sequence or antisense molecule may also be designed to block translation of mRNA by preventing the transcript from binding to ribosomes.

Ribozymes, enzymatic RNA molecules, may also be used to catalyse the specific cleavage of RNA. The mechanism of ribozyme action involves sequence-specific hybridization of the ribozyme molecule to complementary target RNA, followed by endonucleolytic cleavage. For example, engineered hammerhead motif ribozyme molecules may specifically and efficiently catalyse endonucleolytic cleavage of polynucleotide sequences. Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the target molecule for ribozyme cleavage sites, including the following sequences: GUA, GUU, and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides, corresponding to the region of the target containing the cleavage site, may be evaluated for secondary structural features which may render the oligonucleotide inoperable. The suitability of candidate targets may also be evaluated by testing accessibility to hybridization with complementary oligonucleotides using ribonuclease protection assays.

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Complementary ribonucleic acid molecules and ribozymes of the invention may be prepared by any method known in the art for the synthesis of nucleic acid molecules. These include techniques for chemically synthesising oligonucleotides such as solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by in vitro and in vivo transcription of DNA sequences. Such DNA sequences may be incorporated into a wide variety of vectors with suitable RNA polymerase promoters such as T7 or SP6. Alternatively, these cDNA constructs that synthesise complementary RNA, constitutively or inducibly, can be introduced into cell lines, cells, or tissues.

RNA molecules may be modified to increase intracellular stability and half-life. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5'andlor 3' ends of the molecule, or the use of phosphorothioate or 2'O-methyl rather than phosphodiesterase linkages within the backbone of the molecule. This concept is inherent in the production of PNAs and can be extended in all of these molecules by the inclusion of nontraditional bases such as inosine, queosine, and wybutosine, as well as acetyl-, methyl-, thio-, and similarly modified forms of adenine, cytidine, guanine, thymine, and uridine which are not as easily recognised by endogenous endonucleases.

Many methods for introducing vectors into cells or tissues are available and are equally suitable for use, in vivo, in vitro, and ex vivo. For ex vivo therapy, vectors may be introduced into stem cells taken from a patient and clonally propagated for autologous transplant back into that same patient. Delivery by transfection, by liposome injections, or by polycationic amino polymers may

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be achieved using methods which are well known in the art. (See, e.g., Goldman, C.K. et al. (1997) Nature Biotechnology 15:462-466.)

A further embodiment of the present aspect relates to the administration of a pharmaceutical or sterile agent, preferably in conjunction with a pharmaceutically acceptable carrier, for use in a method of prevention or treatment of an inflammatory disease, in particular an eosinophil mediated disease. Such pharmaceutical compositions may consist of polynucleotide, polypeptide, fragments thereof, antibodies, and mimetics, agonists, antagonists, or inhibitors. The compositions may be administered alone or in combination with at least one other agent, drug, or hormone, such as a stabilising compound, which may be administered in any sterile, biocompatible pharmaceutical carrier including, but not limited to, saline, buffered saline, dextrose, and water.

The pharmaceutical compositions utilised in this invention may be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, transdermal, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, or rectal means.

In addition to the active ingredients, these pharmaceutical compositions may contain suitable pharmaceutically-acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. Further details on techniques for formulation and administration may be found in the latest edition of Remington's Pharmaceutical Sciences (Maack Publishing Co., Easton, PA).

Pharmaceutical compositions for oral administration can be formulated using pharmaceutically acceptable carriers well known in the art in dosages suitable for oral administration. Such carriers enable the pharmaceutical compositions to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions, and the like, for ingestion by the patient.

Pharmaceutical preparations for oral use can be obtained through combining active compounds with solid excipient and processing the resultant mixture of granules (optionally, after grinding) to obtain tablets or dragee cores. Suitable auxiliaries can be added, if desired. Suitable excipients include carbohydrate or protein fillers, such as sugars, including lactose, sucrose, mannitol, and sorbitol; starch from corn, wheat, rice, potato, or other plants; cellulose, such as methyl cellulose, hydroxypropylmethyl-cellulose, or sodium carboxymethylcellulose; gums, including arabic and tragacanth; and proteins, such as gelatin and collagen. If desired,

WO 02/10198 PCT/GB01/03390

disintegrating or solubilising agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, and alginic acid or a salt thereof, such as sodium alginate.

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Dragee cores may be used in conjunction with suitable coatings, such as concentrated sugar solutions, which may also contain gum arabic, tale, polyvinylpyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for product identification or to characterise the quantity of active compound, i.e., dosage.

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Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a coating, such as glycerol or sorbitol. Push-fit capsules can contain active ingredients mixed with fillers or binders, such as lactose or starches, lubricants, such as talc or magnesium stearate, and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid, or liquid polyethylene glycol with or without stabilisers.

Pharmaceutical formulations suitable for parenteral administration may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiologically buffered saline. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils, such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate, triglycerides, or liposomes. Non-lipid polycationic amino polymers may also be used for delivery. Optionally, the suspension may also contain suitable stabilisers or agents to increase the solubility of the compounds and allow for the preparation of highly concentrated solutions.

For topical or nasal administration, penetrants appropriate to the particular barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

The pharmaceutical compositions of the present invention may be manufactured in a manner that is known in the art, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping, or lyophilizing processes. The pharmaceutical composition may be provided as a salt and can be formed with many acids, including but not limited to, hydrochloric, sulphuric, acetic, lactic, tartaric, malic, and succinic acid. Salts tend to be more soluble in aqueous or other protonic solvents than are the

corresponding free base forms. In other cases, the preferred preparation may be a lyophilized powder which may contain any or all of the following: 1 mM to 50 mM histidine, 0. 1 % to 2% sucrose, and 2% to 7% mannitol, at a pH range of 4.5 to 5.5, that is combined with buffer prior to use. After pharmaceutical compositions have been prepared, they can be placed in an appropriate container and labelled for treatment of an indicated condition. For administration of polypeptides of the present invention, such labelling would include amount, frequency, and method of administration.

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Pharmaceutical compositions suitable for use in the invention include compositions wherein the active ingredients are contained in an effective amount to achieve the intended purpose. The determination of an effective dose is well within the capability of those skilled in the art. For any compound, the therapeutically effective dose can be estimated initially either in cell culture assays, e.g., of neoplastic cells or in animal models such as mice, rats, rabbits, dogs, or pigs. An animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans. A therapeutically effective dose refers to that amount of active ingredient, for example polypeptide, antibody, agonist, antagonist or inhibitors, which ameliorates the symptoms or condition. Therapeutic efficacy and toxicity may be determined by standard pharmaceutical procedures in cell cultures or with experimental animals, such as by calculating the ED50 (the dose therapeutically effective in 50% of the population) or LD50. (the dose lethal to 50% of the population) statistics. The dose ratio of therapeutic to toxic effects is the therapeutic index, and it can be expressed as the ED5O/LD50 ratio. Pharmaceutical compositions which exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies are used to formulate a range of dosage for human use. The dosage contained in such compositions is preferably within a range of circulating concentrations that includes the ED50 with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, the sensitivity of the patient, and the route of administration. The exact dosage will be determined by the practitioner, in light of factors related to the subject requiring treatment. Dosage and administration are adjusted to provide sufficient levels of the active moiety or to maintain the desired effect. Factors which may be taken into account include the severity of the disease state, the general health of the subject, the age, weight, and gender of the subject, time and frequency of administration, drug combination(s), reaction sensitivities, and response to therapy. Long-acting pharmaceutical compositions may be administered every 3 to 4 days, every week, or biweekly depending on the half-life and clearance rate of the particular formulation.

Normal dosage amounts may vary from about 0. 1 ug to 100,000 ug, up to a total dose of about 1 gram, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature and generally available to practitioners in the art.

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Those skilled in the art will employ different formulations for nucleotides than for proteins or Similarly, delivery of polynucleotides or polypeptides will be specific to their inhibitors. particular cells, conditions, locations, etc.

Any of the therapeutic methods described above may be applied to any subject in need of such 10 therapy, including, for example, mammals such as dogs, cats, cows, horses, rabbits, monkeys, and most preferably, humans.

In another aspect, there is provided a method of diagnosis of diease in a subject, comprising administration to the subject antibodies which specifically bind the polypeptides of the invention. Antibodies may be used for the diagnosis of disorders characterised by expression of polypeptides of the invention, or in assays to monitor patients being treated with polypeptides or agonists, antagonists, or inhibitors. Antibodies useful for diagnostic purposes may be prepared in the same manner as described above for therapeutics. Diagnostic assays include methods which utilise the antibody and a label to detect polypeptide in human body fluids or in extracts of cells or tissues. The antibodies may be used with or without modification, and may be labelled by covalent or non-covalent attachment of a reporter molecule. A wide variety of reporter molecules, several of which are described above, are known in the art and may be used.

A variety of protocols for measuring proteins including ELISAS, RIAS, and FACS, are known in the art and provide a basis for diagnosing altered or abnormal levels of protein expression. Normal or standard values for expression are established by combining body fluids or cell extracts taken from normal mammalian subjects, preferably human, with antibody under conditions suitable for complex formation The amount of standard complex formation may be quantitated by various methods, preferably by photometric means. Expression levels in subject, control, and disease samples from biopsied tissues are compared with the standard values. Deviation between standard and subject values establishes the parameters for diagnosing disease.

In another embodiment, there is provided a method of diagnosis of disease in a subject, the 35 method comprising administration of polynucleotides of the present invention. The

polynucleotides which may be used include oligonucleotide sequences, complementary RNA and DNA molecules, and PNAS. The polynucleotides may be used to detect and quantitate gene expression in biopsied tissues in which expression may be correlated with disease. The diagnostic assay may be used to determine absence, presence, and excess expression of polypeptides of the present invention, and to monitor regulation of expression levels during therapeutic intervention.

In a further embodiment, a method of diagnosis is provided which comprises administration to a subject of probes which are capable of detecting polynucleotide sequences, including genomic sequences, encoding polypeptides of the invention or closely related molecules. Such probes may be used to identify nucleic acid sequences which encode polypeptides of the invention. The specificity of the probe, whether it is made from a highly specific region, e.g., the 5' regulatory region, or from a less specific region, e.g., a conserved motif, and the stringency of the hybridization or amplification (maximal, high, intermediate, or low), will determine whether the probe identifies only naturally occurring sequences encoding polypeptides of the invention, alleles, or related sequences.

Probes may also be used for the detection of related sequences, and should preferably have at least 50% sequence identity to any of the polynucleotide sequences of the present invention. The hybridization probes of the subject invention may be DNA or RNA and may be derived from the sequence of Figure 2, or 4.

Means for producing specific hybridization probes for DNAs include the cloning of polynucleotide sequences of the present invention or derivatives thereof into vectors for the production of mRNA probes. Such vectors are known in the art, are commercially available, and may be used to synthesise RNA probes in vitro by means of the addition of the appropriate RNA polymerases and the appropriate labelled nucleotides. Hybridization probes may be labelled by a variety of reporter groups, for example, by radionucleotides such as P<sup>32</sup>, S<sup>31</sup> or by enzymatic labels, such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, and the like.

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In further embodiments, oligonucleotides or longer fragments derived from any of the polynucleotide sequences described herein may be used as targets in a microarray. The microarray can be used to monitor the expression level of large numbers of genes simultaneously and to identify genetic variants, mutations, and polymorphisms. This information may be used to determine gene function, to understand the genetic basis of a disorder, to diagnose a disorder, and to develop and monitor the activities of therapeutic agents. Microarrays may be prepared,

used, and analysed using methods known in the art. (See, 20 e.g., Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796; Schena, M. et al. (1996) Proc. Natl. Acad. Sci. 93:10614-10619; Baldeschweiler et al. (1995) PCT application W095/251116; Shalon, D. et al. (1995) PCT application W095135505; Heller, R.A. et al. (1997) Proc. Natl. Acad. Sci. 94:2150-2155; and Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662).

The polynucleotide sequences of the present invention may be used in Southern or northern analysis, dot blot, or other membrane-based technologies; in PCR technologies; in dipstick, pin, and ELISA assays; and in microarrays utilising fluids or tissues from patients to detect altered gene expression. Such qualitative or quantitative methods are well known in the art.

In a particular embodiment, the nucleotide sequences of the present invention may be useful in assays that detect the presence of associated disorders, particularly those mentioned above. The nucleotide sequences may be labelled by standard methods and added to a fluid or tissue sample from a patient under conditions suitable for the formation of hybridization complexes. After a suitable incubation period, the sample is washed and the signal is quantitated and compared with a standard value. If the amount of signal in the patient sample is significantly altered in comparison to a control sample then the presence of altered levels of nucleotide sequences in the sample indicates the presence of the associated disorder. Such assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical trials, or to monitor the treatment of an individual patient.

Also envisaged are methods of diagnosis comprising administration to a subject of agents including agonists and antagonists of the polypeptides of the invention, the polypeptides of the invention or fragments thereof, and complements of the polynucleotides of the invention.

The above molecules of the present invention may be used for the diagnosis of eosinophil mediated inflammatory disease. Examples of such disorders include, but are not limited to asthma, emphysemia, COPD, bronchitis, allergic disorders such as atopic dermatitis and NERDS (nodules eosinophilia, rheumatism, dermatitis and swelling); vasculitic granulomatous diseases including polyarteritis, Wegeners granulomatosis; some auto-immune diseases; interstitial and other pulmonary diseases including eosinophilic pneumonia, sarcoiditis and idiopathic pulmonary fibrosis; and neoplastic and myoploriferative diseases including hypereosinophilic syndrome, T cell lymphoma and hodgkins disease.

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In order to provide a basis for the diagnosis of an eosinophil mediated inflammatory disorder, a normal or standard profile for expression is established. This may be accomplished by combining body fluids or cell extracts taken from normal subjects, either animal or human, with at least one sequence, or a fragment thereof, under conditions suitable for hybridization or amplification. Standard hybridization may be quantified by comparing the values obtained from normal subjects with values from an experiment in which a known amount of a substantially purified polynucleotide is used. Standard values obtained in this manner may be compared with values obtained from samples from patients who are symptomatic for a disorder. Deviation from standard values is used to establish the presence of a disorder. Once the presence of a disorder is established and a treatment protocol is initiated, hybridization assays may be repeated on a regular basis to determine if the level of expression in the patient begins to approximate that which is observed in the normal subject. The results obtained from successive assays may be used to show the efficacy of treatment over a period ranging from several days to months.

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A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the disease.

Additional diagnostic uses for polynucleotides of the present invention may involve the use of 20 PCR. Oligomers may be chemically synthesised, generated, enzymatically, or produced in vitro. Oligomers will preferably contain a fragment of a polynucleotide of the present invention, or a fragment of a polynucleotide complementary thereto, and will be employed under optimised conditions for identification of a specific gene or condition. Oligomers may also be employed 25 under less stringent conditions for detection or quantitation of closely related DNA or RNA sequences. Methods which may also be used to quantitate expression include radiolabelling or biotinylating nucleotides, coamplification of a control nucleic acid, and interpolating results from standard curves. (See, e.g., Melby, P.C. et al. (1993) J. Immunol. Methods 159:235-244; and Duplaa, C. et al. (1993) Anal. Biochem. 229-236). The speed of quantitation of multiple samples 30 may be accelerated by running the assay in an ELISA format where the oligomer of interest is presented in various dilutions and a spectrophotometric or calorimetric response gives rapid quantitation.

In another aspect of the present invention, polynucleotide sequences of the invention may be used to generate hybridisation probes useful in mapping the naturally occurring genomic sequence. The sequences may be mapped to a particular chromosome, to a specific region of a

chromosome, or to artificial chromosome constructions, e.g., human artificial chromosomes (HACs), yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial PI constructions, or single chromosome cDNA libraries. (See, e.g., Price, C.M. (1993) 30 Blood Rev. 7:127-134; and Trask, B.J. (1991) Trends Genet. 7:149-154).

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Fluorescent in situ hybridization (FISH) may be correlated with other physical chromosome mapping techniques and genetic map data. (See, e.g., Heinz-Ulrich, et al.(1995)in Meyers, R.A. (ed.) Molecular Biology and Biotechnology, VCH Publishers New York, NY, pp.965-968). Examples of genetic map data can be found in Various scientific journals or at the Online Mendelian Inheritance in Man (OMB4) site. Correlation between the location of the gene on a physical chromosomal map and a specific disorder, or a predisposition to a specific disorder, may help define the region of DNA associated with that disorder. The nucleotide sequences of the invention may be used to detect differences in gene sequences among normal, carrier, and affected individuals.

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In situ hybridization of chromosomal preparations and physical mapping techniques, such as linkage analysis using established chromosomal markers, may be used for extending genetic maps. Often the placement of a gene on the chromosome of another mammalian species, such as mouse, may reveal associated markers even if the number or arm of a particular human chromosome is not known. New sequences can be assigned to chromosomal arms by physical mapping. This provides valuable information to investigators searching for disease genes using positional cloning or other gene discovery techniques. Once the disease or syndrome has been crudely localised by genetic linkage to a particular genomic region, any sequences mapping to that area may represent associated or regulatory genes for further investigation. (See, e.g., Gatti, R.A. et al. (1988) Nature 336:577-580). The nucleotide sequence of the subject invention may also be used to detect differences in the chromosomal location due to translocation, inversion, etc., among normal, carrier, or affected individuals.

In yet another aspect of the invention, there is provided a transgenic non-human animal comprising a polynucleotide sequence according to the second or third aspects of the invention. The transgenic non-human animal may comprise a polypeptide according to the first aspect of the invention.

In further aspects, the polynucleotide or polypeptide sequences of the present invention may be used in any molecular biology techniques that have yet to be developed, provided the new

techniques rely on properties of nucleotide sequences that are currently known, including, but not limited to, such properties as the triplet genetic code and specific base pair interactions.

The present invention may be better understood by reference to the following non-limiting

Examples, which are provided as exemplary of the invention. The present invention is not to be limited in scope by the specific embodiments described herein. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and the accompanying figures. Such modifications are intended to fall within the scope of the invention.

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It is further to be understood that all base sizes or amino acid sizes, and all molecular weight or molecular mass values, given for nucleic acids or polypeptides are approximate, and are provided for description.

#### **EXAMPLES**

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# Example 1: Cloning of Human Eosinophil cDNA

This example describes the cloning of polynucleic acids expressed by human peripheral blood eosinophils.

# Example 1.1: Purification of Human Peripheral Blood Eosinophils

Eosinophils were purified from 200ml whole blood essentially as described by Dubois et al., Am. J. Respir. Cell Mol. Biol., 1998. Essentially, the blood was layered on to Accuspin tubes with filter histopaques (Sigma) and centrifuged (2100rpm) for 20 minutes. The Peripheral Blood Mononuclear Cell (PBMC) layer was carefully removed and the filters washed twice with PBS. The filters were punctured and the blood (approx.15ml) under each filter was transferred to sterile 50ml tubes. The lysis of the red blood cells was performed as follows: 6% dextran (6ml) and PBS (44ml) were added to each tube, the lysis solution was mixed by inverting and left to incubate for 45 min. at room temperature (RT). The supernatants were subsequently collected, pooled and centrifuged (1,600rpm) for 5 min. The resultant pellet was resuspended in PBS (5ml) and hypotonic shock was performed to completely remove the red blood cell contamination from the granulocyte layer. The granulocytes were incubated with anti-CD16 beads (Dynal, Norway) for 40 min. at 4°C and the eosinophils subsequently purified from the neutrophils by negative selection.

# Example 1.2: Extraction of Total Cellular RNA

Total cellular RNA was extracted from the eosinophils using essentially the modified RNAzolB method described by Kodavanti et al. Exp. Lung Res., 1996. Total cellular RNA quality was assessed by electrophoresis through formamide/formaldehyde TAE gels, as described in (Maniatis T. et al., "Molecular Cloning, a Laboratory Manual," Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y., 1982; Ausubel F.M. et al. (eds.), "Current Protocols in Molecular Biology," John Wiley & Sons, New York, 1987). Both 28 S and 18S fibosomal RNAswere detected as shown in figure 1. 30

# Example 1.3: Extraction of polyA+ mRNA

Poly(A) mRNA was purified from total RNA using a Micro poly A+ kit (Ambion), according to the manufacturers protocol.

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# Example 1.4: Production of PCR amplified cDNA

cDNA was synthesised from 400ng human eosinophil mRNA SMART PCR cDNA Synthesis Kit (Clontech). The methodology used was essentially as described by the manufacturer, with the following modifications: the two 5' and 3' SMART oligonucleotide primers, respectively, were replaced by modified HPLC purified primers having the sequence shown in figure 4. These primers contain essentially the same amplification and Poly dT sequences described by the manufacturers Clontech. The RsaI restriction sites are replaced by AscI and NotI restriction sites. These new restriction sites, allow directional cloning, but also have 8-base pair enzyme recognition sequences. 8-base pair recognition sequences are rare in mammalian genes, consequently cDNA sequences are unlikely to be digested internally with the use of these enzymes. The size range of the amplified cDNA was between 200bp and 7kb as shown in figure 2.

# 15 Example 1.5: Modification of cDNA library cloning vector

The vectors pSKII (Stratagene) was modified by the inclusion of additional 8bp sites (AscI and PacI). The vector was digested PstI/EcoRI and ligated with dephosphorylated double stranded oligonucleotides to generate the additional 8bp sites shown in figure 5. The genetic engineering techniques used to clone and insert cDNAs into these plasmids employed routine protocols described in Maniatis, 1989.

### Example 1.6: cDNA Library Construction

PCR amplified cDNA (approx. 15μg) was digested with NotI and AscI, and size fractionated on a Sephacryl S-500 gel filtration column (Gibco BRL Life Technologies), as described by the manufacturer. Fractions containing cDNA >500bp were combined and ligated. All ligations were performed in 20μl reaction volume using 50ng modified pBluescript SK II (+) vector, 80ng cDNA and 1 unit of T4 DNA Ligase (Gibco BRL Life Technologies), and incubated at 16°C O/N. Ligation reactions were purified (phenol/chloroform extraction and ethanol precipitated, as described in Maniatis, 1989) and used to transform *E. Coli* TG1 cells (supE, hsdD5, thi, D(lac-proAB), F'(tra D36 pro A<sup>+</sup>B<sup>+</sup> lacI<sup>q</sup> lacZDM15), Stratagene) by electrophoration as follows: TG1 cells were thawed on ice and mixed with 1μl ligated DNA. The cell/DNA mixture was transferred to a chilled electroporation cuvette (0.1 cm; BIORAD) and pulsed for 4 seconds at (1700V, 200A, 25μF; Gene Pulser II; BIO RAD). SOC (960μl) was added to resuspend the cells, and the suspension incubated at 37°C for 1h. Transformed cells are plated onto LB Agar (L-broth: NaCl (5 g/l), Bacto-tryptone (10 g/l), Yeast extract (5 g/l);

Difco), containing ampicillin, under blue/white selection. The library contained  $> 1 \times 10^6$ independent clones, with an average insert size range of 400bp to 2.5kb as determined by restriction digest.

# Example 1.7: Normalisation of cDNA Library

Plasmid DNA from the eosinophil cDNA library (50µg) was digested with AscL/NotI restriction enzymes and the insert fragments isolated by gel purification (called 'Tracer'). Purified PCR products which had been amplified (using T7/T3 primer sequences) from 5000 eosinophil miniprep cDNA clones were pooled and photobiotinylated ('Driver'). The methodology for photobiotinylation and subtraction, was essentially as described by Wang, Z and Brown, DD; Proc Natl Acad Sci USA 1991 Dec 15;88(24):11505-9. Two rounds of hybridisation/subtraction (68°C, 20h) with 100:1 biotinylated Driver:Tracer ratio are carried out. Hybrids were removed with Streptavidin and extracted 5 times with phenol/chloroform. The enriched Tracer DNA was ethanol precipitated, ligated into modified pSK II and transformed in E Coli TG1 cells by electroporation (as described in Example 1.6).

# Example 1.8: Purification of Plasmid DNA

Plasmid DNA clones was purified on a Qiagen 9600 Robot, using Qiaprep 96 Turbo kits (Qiagen), as described by the manufacturer.

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# Example 2: High Throughput Sequencing

This example describes determination of the complete/partial DNA sequence of each isolated cDNA clone. The cDNA was sequenced, using an Applied Biosystems 377 or 373 DNA Sequencing System, using the Prism Big Dye Terminator Cycle Sequencing chemistry (PE-BioSystems). The modified pBluescriptIISK/cDNA insert clones are sequenced on the 5' and the 3' vector strand using the T3 promoter primer (5'AATTAACCCTCACTAAAGGG3') and the T7 promoter primer, respectively (5'TAATACGACTCACTATAGGG3'). Where necessary the cDNA was sequenced internally using primers based on previous sequencing results, essentially following the same protocols.

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# Example 3: Database Search and Sequence Annotation

This example describes searching the publicly available databases GenBank, SwissProt, TrEMBL (Bairoch A., Apweiler R., "The SWISS-PROT protein sequence data bank and its supplement TrEMBL", Nucleic Acids Res 1999 Jan 1;27(1):49-54) and PFAM (Bateman A, etal. "Pfam 3.1: 1313 multiple alignments and profile HMMs match the majority of proteins", Nucleic Acids Res. 1999 Jan 1;27(1):260-2.). GenBank is the NIH genetic sequence database,

an annotated collection of all publicly available DNA sequences (Nucleic Acids Research 1999 Jan 1;27(1):12-7) and has been searched for certain of the nucleotide sequences of the invention, which correspond to the determined DNA sequences for each isolated cDNA clone, to ensure the novelty of these sequences. Additional sequencing has been performed for sequence elongation, sequence assembly and sequence verification. Functional annotation in silico may be performed to search the deduced protein sequences for protein domains and similarities to known protein sequences.

The base-calling program Phred (Ewing B. et al., "Base-calling of automated sequencer traces using phred. II. Error probabilities", Genome Res 1998 Mar;8(3):186-94) was used to analyse the DNA sequence traces, to deduce nucleotide sequences and to assign quality scores for each individual nucleotide of these sequences. The derived sequences covering the 5' end of each clone insert were compared versus the GenBank databases version 111 for primate sequences and version 110 for pubESTs, respectively using the BLAST database search program version 2.0.8 (Altschul, S. et al., "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res 1997 Sep 1;25(17):3389-402). In order to identify and mask repetitive regions all query sequences were firstly compared against a database containing a collection of human repetitive sequences called REPBASE (Prepared for National Center for Biotechnology Information Contract No. N01-LM-2-3526 P.I. Jerzy Jurka, Linus Pauling Institute of Science and Medicine 440 Page Mill Rd Palo Alto, CA 94306). The XBLAST software (Claverie J. M. and States D. J. "Information Enhancement Methods for Large Scale Sequence Analysis", Computers and Chemistry 1993, 17: 191-201.) was used to mask all regions with homology to any of those repeat sequences. Functionally, XBLAST reads a BLAST output file and generates query sequences where all segments with hits are masked. BLAST version 2.0.8 was used for subsequent database searches of these masked query sequences against all database entries of the GenBank databases version 111 for primate sequences and version 110 for pubESTs and to evaluates the statistical significance of detected sequence similarities.

None of the polynucleotide sequences filed here showed significant homology in GenBank databases version 111 for non-genomic primate (pri) sequences and version 110 for public EST sequences (pubEST). All these sequences were found to be above the user-selected threshold of significance (BLAST e-value) of 10.sup.-7 and are therefor assumed to represent novel human cDNA sequences.

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144 cDNA clones were elongated by generating the 3' sequence for each clone. The corresponding 5' and 3' read of each clone insert was assembled utilising the Phrap software ("phragment assembly program", or "phil's revised assembly program"; ©1994-1999 by Phil Green, University of Washington) and the resulting sequence assemblies ("contigs") were manually edited in the Consed sequence editor (Gordon D. etal., "Consed: a graphical tool for sequence finishing", Genome Res 1998 Mar;8(3):195-202) to increase the accuracy of the deduced consensus sequences. These derived consensus sequences correspond to the full-length insert of each cDNA clone. The resulting sequences correspond to Seq Id Nos: 1-466 (polynucleotide) all of which are at least 200 nucleotides in length, and include no more than 8% of uncalled bases (where N is recorded rather than A, C, G, or T).

For functional annotation in silico the deduced protein sequence may be examined using different approaches to detect remote homologies to characterised protein sequences and similarities to known protein domains. These methods include sequence comparisons against different databases including GenBank and PFAM (Bateman A, et al. "Pfam 3.1: 1313 multiple alignments and profile HMMs match the majority of proteins", Nucleic Acids Res. 1999 Jan 1;27(1):260-2.) and sensitive search algorithms using iterated sequence database search methods (Taylor WR, et al. "Iterated sequence databank search methods." Comput Chem. 1999 Jun 15;23(3-4):365-85.) and profile hidden Markov models for the detection of distant sequence homologs and low conserved protein domains (Eddy SR, et al., "Maximum discrimination hidden Markov models of sequence consensus", J Comput Biol. 1995 Spring;2(1):9-23.).

For the sequence listing the most 5-prime region of each sequence has been translated in all three possible reading frames and specified whenever the deduced product resulted in a hypothetical peptide of more then 9 amino acids. Additional 5-prime sequence information can be unravelled in order to define the correct and full length coding sequence.

Example 4: Construction and Use of Microarray, for Amersham Microarray System

This example describes the use of a microarray system developed and commercialised

(Amersham Pharmacia Biotechnology). This methodology, essentially using protocols

pioneered by Pat Brown and colleagues (Schena, M et al. Quantitative monitoring of gene
expression patterns with a complementary DNA microarray. Science 270, 467-470 (1995).

cDNA fragments of up to 2.5kb in length were amplified by PCR from the eosinophil cDNA clones. PCR reactions (100 µl) were performed in 1x Taq DNA Polymerase buffer using 2.5 U Taq DNA polymerase (Qiagen), 100 mM dNTPs and 400 nM each of T7 and T3 primers 1T7 primer: 5'GTAATACGACTCACTATAGGGC3', T3 primer:

5'AATTAACCCTCACTAAAGGG3']. PCR was performed in 96 well microtitre plates with a 1 min denaturation step at 94°C, 36 rounds of amplification (denaturation 94°C, 40 sec, annealing 55°C, 30 sec, extension 72°C, 2 min), followed by a 2min extension step at 72°C.

#### Example 4.2: Purification, QC and Quantitation of PCR Products

Quadruplicate 100µl PCR reactions were pooled and purified on a Biorobot-9600 (Qiagen) using the Qiaquick 96 PCR Biorobot kit (Qiagen). 100µl of PCR reactions were mixed with 500µl of buffer PB and applied sequentially to Qiaquick modules until the 4 replicate reactions had been applied to a single well. Qiaquick modules were washed with 2 x 750µl of PE per well, dried using the vacuum manifold and DNA was eluted with 80µls of water into 96 well microtitre plates.

DNA was quantitated using the fluorescent reagent Sybrgreen (Molecular Probes). 300µl of a 1:3000 of the Sybrgreen dye was mixed with 1µl of purified DNA in a 96 well white Opti plate (Packard). Fluorescence was measured, using a Victor plate reader (Wallac), at an excitation wavelength of 495nm and an emission wavelength of 520nm. A standard curve was constructed using a plasmid DNA dilution series; the concentrations of which were determined by Absorbance at 260nm.

All purified DNA samples were analysed by agarose gel electrophoresis to verify that PCR fragments of a size consistent with the sequencing analysis for that clone (see example 2) had been generated. Samples were dried in a centrifugal evaporator (Savant) and reconstituted to 500 ng/µl in 50% (v/v) DMSO. 20µl of sample /well was transferred from 4 (96 well) microtitre plates to a 384 well microtitre plate for spotting onto microarray slides.

#### 30 Example 4.3: Spotting of Microarray

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DNA was spotted onto Type 7 mirrored slides (Amersham) using the GenIII microarray spotter (Amersham), using conditions essentially as described by the manufacturer. Humidity was controlled within the spotter at 55%. Normal mode spotting was employed which produced replicate arrays on the right and left side of each slide. UV crosslinking of the DNA onto the slides was achieved using a CL-100 Ultraviolet Crosslinker (UVP) set at 100mJ/cm<sup>2</sup>. Slides were stored dessicated in the dark until use.

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# Example 4.4: Preparation of Fluorescently labelled Samples

#### Example 4.4.1: RNA preparation

RNA was prepared from either primary cells (e.g. eosinophils) or from cell lines (e.g. A549 human lung epithelial cells). Total RNA was isolated from cell lines using the RNeasy kit (Qiagen), using procedures as described by the manufacturer. RNA was isolated from primary cells using the modified RNAzolB method described by Kodavanti et al. Exp. Lung Res., 1996. Total RNA integrity was assessed by denaturing agarose gel electrophoresis, as described in Example 1.2. RNA was quantified by Abs 260nm determination.

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Poly(A+) mRNA was purified from total cellular RNA using a Micro poly A+ kit (Ambion), according to the manufacturer's protocol.

#### Example 4.4.2: Labelled cRNA Samples

1 μg of mRNA and 100 pmoles of T7-(dT)<sub>24</sub> were denatured at 70°C for 10min in a volume 15 of 13ul. DTT, dNTPs and 5X 1st strand buffer were added to 10mM, 0.5mM and 1X respectively, and incubated in a total volume of 20µl for 2 min at 37°C. Reverse transcription was initiated by addition of 1µl of 200 U/µl superscript II enzyme ( Gibco BRL Life Technologies) and incubating at 37°C for 1 h. Second strand cDNA synthesis was initiated by addition of 1µl of 10U/µl DNA Ligase (Gibco BRL Life Technologies), 4µl of 10U/µl DNA 20 Polymerase I (Gibco BRL Life Technologies), 1µl of 2U/µl RNase H (Gibco BRL Life Technologies) and incubated in a total volume of 150µl for 2 hours at 16°C. After this incubation 2µl of 5U/µl T4 DNA Polymerase was added and incubated for 5 minutes at 16°C. 10µl of 0.5M EDTA was added to the double stranded cDNA. The cDNA was, phenol/chloroform extracted, ethanol precipitated, washed with 70% ethanol and air dried. 25 0.5-1µg of linearised T7 cDNA template was reconstituted in a volume of 2µl of DEPC water (Ambion). T7 10X reaction buffer (Ambion), rA/C/GTP, rUTP and rcyUTP (either Cy3 labelled CTP or Cy5 labelled CTP, Amersham) were added to 1X, 150nmoles, 100nmoles and 30nmoles respectively. In-vitro transcription was initiated by adding 2µl of T7 RNA Polymerase (Ambion) and incubated in a total volume of 20µl for 6 hours at 37°C. After this 30 incubation the DNA template was removed by addition of 1µl of RNase-free DNase (Ambion) and incubated for 15 min at 37°C. The labelled cRNA sample was then purified using a

RNeasy purification kit (Qiagen), essentially as described by the manufacturers but with two

sample was, quantitated by Abs260nm, aliquoted into amounts corresponding to 2µg of cRNA

washes with PE buffer and elution with 2x 40µl of DEPC water. The resultant purified

per tube and dried in a centrifugal evaporator (Savant model SC110). Sample was stored at - 20°C in the dark until ready to use in the hybridisation.

#### Example 4.4.3: Labelled cDNA Samples from Total RNA

25 μg of total RNA and 1μg of Oligo dT (Amersham) were denatured at 70°C for 10 minutes in a volume of 11μl. DTT, dNTPs, dcyCTP (either Cy3 labelled CTP or Cy5 labelled CTP, Amersham) and 5X 1<sup>st</sup> strand buffer were added to 10mM, 0.1mM, 62nM and 1X respectively, and incubated in a total volume of 19μl for 10 min at 22°C. Reverse transcription was initiated by addition of 2ul of 200U/μl superscript II enzyme (Gibco BRL Life Technologies) and incubating at 42°C for 2.5 h. After this incubation the cDNA sample was ethanol precipitated, washed with 70% ethanol, air dried and resuspended in 40μl of water. The cDNA:mRNA hybrid was denatured by addition of NaOH to 250mM and incubating at 37°C for 10 min. The hydrolysis was terminated by neutralisation with 6μl of IM Hepes pH 8. The labelled cDNA sample was then purified using a PCR purification kit (Qiagen), essentially as described by the manufacturers but with two washes with PE buffer and elution with 2x 30μl of 10mM Tris pH 8.5. The resultant purified sample was aliquoted into amounts corresponding to preparations from 10μg of total RNA per tube and dried in a centrifugal evaporator (Savant). Sample was stored at -20°C in the dark until ready to use in the hybridisation

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#### Example 4.4.4: Labelled cDNA Samples from mRNA

cDNA samples prepared from mRNA were made using essentially the same procedure detailed in section 4.4.3 but using 2.5  $\mu$ g of mRNA instead of 25  $\mu$ g of total RNA. Sample was aliquoted at the final stage into amounts corresponding to preparations from 1  $\mu$ g of starting mRNA per tube.

### Example 4.5: Hybridisation of Microarray

#### Example 4.5.1: Pre-treatment of microarray slides

Microarrayed slides (Example 4.3) are pre-treated by incubating in 5xSSC/0.2% SDS for 2 h at 60°C. Slides are washed 5x in distilled water, 2x in isopropanol and dried rapidly using a compressed air can.

#### Example 4.5.2: Hybridisation

Hybridisation mixtures for a single slide were prepared as follows. An aliquot of labelled sample (prepared as described in Examples 4.4.2, 4.4.3 or 4.4.4) was reconstituted in 6.7 µl of water, denaturing at 95°C for 2 min and then incubated on ice for 2 min. The sample was the added to a hybridisation mix that had been pre-equilibrated at 42°C to give final concentration of 3µg/ml Oligo A80, 50% formamide in 1x Type II hybridisation buffer (Amersham). The total volume of the hybridisation mixture was 40µl per slide and this was applied to the pre-treated microarray slides and incubated under a coverslip (22mm x 65mm), in a humid chamber at 42°C overnight.

#### 10 Example 4.5.3: Post Hybridisation washes

Post hybridisation washes were performed at 55°C as follows.

Wash 1 - 5 min wash in 1xSSC/0.2% SDS for 5 min

Wash 2- 10 min wash in 0.1xSSC/0.2% SDS

Wash 3-10 min wash in 0.1xSSC/0.2% SDS

15 Wash 4- 10 min wash in 0.01xSSC/0.1%SDS

Slides are rinsed with distilled water, dried rapidly with compressed air.

#### Example 4.6: Scanning of Microarray

The fluorescence of each spot was determined by scanning the slides in a GenIII microarray scanner (Amersham). Cy3 fluorescence was determined using an excitation wavelength of 532nm and an emission wavelength of 575nm. Cy5 fluorescence was determined using an excitation wavelength of 633nm and emission wavelength of 675nm. PMT values are set over a range 675-750 V.

#### 25 Example 4.7: <u>Data Capture</u> and <u>Processing</u>

Images of scanned slides are analysed using ArrayVision software (Imaging Research). Expression values for each gene are determined from the fluorescence contained in a circle around each spot and a correction applied for the background fluorescence on the slide.

#### 30 Example 5: Construction and Use of Affymetrix Custom Probe Array

This example describes the design of a customised Affymetrix probe array, using DNA sequences of isolated cDNA clones. This example also describes the methodology for use of the custom probe array. This technology is referenced through the following patents/submissions: PCT/US98/22966, PCT/US98/01206, 5,800,992 patent and PCT/US94/07106.

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All sequences were screened for low complexity regions and repetitive sequences and vector contamination's using Swat and cross-match (Copyright (C) 1994-1999 by Phil Green, University of Washington) which are based on an efficient implementation of the Smith-Waterman-Gotoh algorithm (Waterman MS, "Efficient sequence alignment algorithms", J Theor Biol. 1984 Jun 7;108(3):333-7).

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Repetitive regions of all sequences were masked prior to sequence submission to Affymetrix by comparing all sequences against REPBASE a database containing a collection of human repetitive sequences (prepared for National Center for Biotechnology Information Contract No. N01-LM-2-3526 P.I. Jerzy Jurka, Linus Pauling Institute of Science and Medicine 440 Page Mill Rd Palo Alto, CA 94306) using BLAST version 2.0.8 (Altschul, S. et al., "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res 1997 Sep 1;25(17):3389-402) in combination with the XBLAST software (Claverie J. M. and States D. J. "Information Enhancement Methods for Large Scale Sequence Analysis", Computers and Chemistry 1993, 17: 191-201.). XBLAST reads each BLAST output file and generates a sequence where all segments with hits against the repeat database have been masked. This masked sequences provides better templates for the probe design because nonspecific regions shared by several genes have been excluded from the submitted sequences and less unwanted cross-hybridisation's will affect the experimental results obtained with the final micro-arrays.

#### Example 5.2: Labelled Sample synthesis, Hybridisation and Scanning

The methodology describing the sample synthesis, hybridisation and scanning etc. for the probe array is described in detailed protocols supplied by Affymetrix. Essentially, poly(A+) mRNA is extracted and purified form total cellular RNA (5 to 100µg) using a Micro poly(A+) kit (Ambion). The synthesis of cDNA (from 0.5-5µg mRNA) is using the Superscript Choice system kit (Gibco BRL Life Technologies), and incorporated a T7-(dT)24 primer (GENSET). Purified cDNA (upto 2µg) is in-vitro transcribed using the MEGAscript T7 Kit (Ambion), and incorporates Biotin-11-CTP and Biotin-16-UTP (final conc. 1.875mM; Sigma/Enzo). Following purification, IVT cRNA is fragmented in a magnesium containing buffer at 94°C. A hybridisation mix, containing cRNA, herring sperm DNA, acetylated BSA and a MES-based buffer, is denatured and then incubated onto the probe array at 45°C, rotating at 60rpm, for approx. 16h. Following incubation, the hybridisation mix is removed and the probe arrays washed using the Affymetrix Fluidics Station. Whilst remaining on the Fluidics Station, the probe array is stained with Streptavidin Phycoerythrin (SAPE; final conc. 10µg/ml; Molecular Probes). For probe arrays having a 24 $\mu$ m x 24 $\mu$ m feature size, an additional

antibody amplification, washing and staining step is used, as follows: Following the first addition of SAPE (10 min. 25°C), the probe array is washed and then incubated with a solution containing biotinylated anti-streptavidin antibody (Vector Laboratories; 10 min. 25°C). After a further cycle of washing the probe array is stained a second time with SAPE (10 min. 25°C). The probe array is scanned, after the wash protocols are complete, using the Affymetrix scanner (570nm).

Example 5.3: Data Capture and Processing

After scanning the probe array, the resulting image data created is stored as a .dat file. In the first step of the analysis, a grid is automatically placed over the .dat file so that it demarcates each probe cell. A probe array library file (.cif, supplied by Affymetrix), defines the identity and location of each gene probe. The scanned image is then analysed using the Affymetrix GeneChip software, which generates an exportable .txt file containing expression information and characteristics for each DNA sequence represented upon the probe array as shown in Figure X.

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WO 02/10198 68

#### Example 6: Details of Experiments for Microarray Profiling

There are many ways microarrays can be used to produce functional annotation of the genes included on the array. The following examples describe different experiments conducted to profile mRNA expression levels using microarrays (Affymetrix and Amersham type). Such experiments form part of the strategy to identify candidate target genes (such techniques are review in the Supplement to Nature Genetics. 21: 1999).

#### Example 6.1: Tissue Distribution

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10 The example describes the characterisation of the expression specificity of genes, characterised by the isolated cDNA clones. Such a pattern provides indirect information about function. A gene expressed exclusively in cosinophils is likely to be involved in pathologies associated with the eosinophil such as inflammatory disease such as asthma. Effective drugs have been developed against protein targets widely expressed in the body. However, highly selective tissue expression of a drug target is attractive, as the potential for 15 unwanted side effects may be more restricted. Knowledge of highly selective gene expression, alongside other information on a gene, can thus provide a shortcut for implicating a target in a given pathway or disease.

#### Example 6.1.1: Commercial Human Tissue poly(A+) mRNA

Labelled samples are synthesised from human tissue poly(A+) mRNA obtained from commercial sources (Clontech, InVitrogen). Tissues include, bone marrow, liver, kidney, brain and lung.

#### 25 Example 6.1.2: Purified Human Leukocytes

Labelled samples are synthesised from poly(A+) mRNA extracted and purified from human leukocytes. Human leukocyte preparations are purified from peripheral blood essentially as described for eosinophils, and include: eosinophils, neutrophils, mononuclear cells, T cells and B cells. In some cases the purified leukocytes are stimulated/activated overnight prior to isolation of mRNA e.g. T cells treated with anti-CD3 and anti-CD28 antibodies, or B cells treated with IL-4 and anti-CD40 antibody.

#### Example 6.2: Cell Based Models of Eosinophil Function

The examples describe the characterisation of the expression pattern of genes, included on the microarray, in primary cells isolated from normal and diseases humans as well-as model cellular systems. Discrete aspects of cellular function can be biochemically and physiologically

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modelled in cell lines (e.g. chemotaxis or adhesion in response to physiological cytokines). Detailed profiling of gene expression in model cell lines yields dissection of the critical pathways and cellular responses, and highlights key targets. The example describes the characterisation of the expression pattern of genes, identified from the isolated cDNA clones, in cell based model systems. Such systems provide ideal models for the functional validation of candidate targets prior to further characterisation and validation in animal models etc.

# Example 6.2.1: IL-5 Treatment of Primary Human Eosinophils

IL-5, like its related cytokines GM-CSF and IL-3, is a key mediator in many aspects of eosinophil functional biology (Devos R etal. *J Leukoc Biol.* 1995 Jun;57(6):813-9, Okudaira H etal. *Int Arch Allergy Immunol.* 1998 Sep;117(1):11-9). Genes which are regulated in eosinophils following treatment with IL-5 might be expected to have a role in eosinophil function.

Human peripheral blood eosinophils were isolated, as described (Example 1.1), and treated with medium containing IL-5 (1 to 100pM; R&D Systems) or media alone as a control. Following treatment (1h to 18h time points), RNA was extracted as described (Example 1.2).

# Example 6.2.2: <u>IL-5 and GM-CSF Treatment of a Human Eosinophil-Like Cell Line:</u> AML14.3D10

The AML14.3D10 cell line has been identified and characterised as a surrogate model cell line resembling the human eosinophil (Baumann MA et al. Stem Cells. 1998;16(1):16-24, Paul CC et al. Blood. 1993 Mar 1;81(5):1193-9). Genes which are regulated in AML14.3D10 following treatment with IL-5 and/or GM-CSF might be expected to have a role in eosinophil function.

AML14.3D10 cells are cultured, as described in Example 8, and treated with medium containing IL-5 or GM-CSF (1 to 100pM; R&D Systems) or media alone as a control. Following treatment (1h to 18h time points), RNA is extracted as described (Example 1.2).

#### Example 6.2.3: Adhesion of AML14.3D10 to Fibronectin

The critical process of adhesion by an eosinophil has been modelled in AML14.3D10. The model system is described in detail in Example 8. Following adhesion (approx. 1h), the adherent and non-adherent AML14.3D10 cell populations were harvested and RNA were extracted as described (Example 1.2). In some experiments, non-adherent cells are harvested at time points upto 48h post-adhesion.

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# Example 6.2.4: IL-5 Withdrawal from IL-5-dependent Cell Line: TF1.8

Withdrawal of IL-5 from the IL-5-dependent Cell Line: TF1.8 is described in Example 8 relating to Validation. Following IL-5 withdrawal (time points between 15 min. and 48h), cells are harvested and RNA is extracted as described (Example 1.2).

# Example 6.2.5: <u>Eotaxin Treatment of Primary Human Eosinophils and AML14.3D10 Cells</u> Expressing Human Eotaxin Receptor CCR3

As eotaxin, is a key mediator in many aspects of cosinophil functional biology (Graziano

FM etal. Allergy Asthma Proc. 1999 May-Jun;20(3):141-6, Corrigan CJ etal. Clin Exp

Immunol. 1999 Apr;116(1):1-3). Genes which are regulated in cosinophils following treatment with cotaxin might be expected to have a role in cosinophil function.

Human peripheral blood eosinophils, or AML14.3D10 cells, isolated and cultured respectively, as described (Example 1.1 and 8.5), were treated with medium containing eotaxin (1 to 100pM; R&D Systems) or media alone as a control. Following treatment (1h to 18h time points), RNA was extracted as described (Example 1.2).

# Example 6.3: Clinical Study with Peripheral Blood Eosinophils from Normal and Asthmatic Individuals

This example describes mRNA expression profiling for human peripheral blood eosinophils from normal and asthmatic individuals from a defined clinical background.

Diversion from normal physiology is frequently accompanied by histological and biochemical changes, including changes in gene expression. The up- or down-regulation of gene activity can either be the cause of the pathophysiology or the result of the disease. The comparison of expression of thousands of genes between 'disease' and 'normal' tissues and cells allows the identification of multiple potential drug targets. Targeting disease-causing gene products is desirable to achieve disease modification, while targeting genes that are expressed as a consequence of disease can lead to alleviation of symptoms.

The following groups are identified and clinically characterised:

- 1. controls normal volunteers
- 35 2. atopic non asthmatic volunteers
  - 3. mild atopic asthmatics >80% predicted FEV1

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- 4. moderate atopic asthmatics 60-80% FEV1
- 5. severe asthmatics (atopic or otherwise) < 60% FEV1.
- 6. atopic: positive skin and rast test. PC20 histamine, > 2mgs//ml
- 7. asthmatic: hyper-responsiveness, PC20 histamine, < 8mgs/ml, wheeze, cough,
- 5 bronchodilator reversible, probably atopic.

RNA was extracted as described (Example 1.2).

# Example 7: Data Normalisation, dB Storage and Visualisation

This example describes the process by which expression data (typically .txt files) from Amersham or Affymetrix microarray experiments was normalised, stored and visualised.

#### Example 7.1 Data Normalisation

Data was normalised using a number of methods depending on the type of data that is being processed. The first method involves a global normalisation method where the total intensity for all genes on the microarray was scaled to the same overall level to give a scale factor that is used for all genes on the microarray; this is done for all microarrays within a single experiment. This method works particularly well when comparing changes within a single cell type under various conditions or where it is expected that only a small number of genes will change from experiment to experiment.

The second method involves normalising based upon the use of genes that are known to be invariant under most cellular conditions (house-keeping genes) such as GAPDH (GlycerAldehyde 3-Phosphate DeHydrogenase), actin or certain ribosomal proteins. For this approach, the levels of the house-keeping gene being used are scaled to the same value for all microarrays within a single experiment giving scale factors that can be used for all other genes on those microarray experiments. This method works well where a large number of genes are expected to change within the experiment.

The final method scaled all the expression levels of the genes on the microarray, in each experiment to a common data set, such as that obtained in an experiment performed on liver cells. The genes used for normalisation are those found to be present within the liver, with the exclusion of the top 10%. The ratios of the expression levels of each of these genes are calculated with respect to the liver experiment, the geometric mean taken and used to normalise the data sets. This approach has the advantage of being used in the large majority of experiments and can be used for cross-tissue comparisons.

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#### Example 7.2 Data-Base Storage and Visualisation of Data

The data is stored in a relational database (such as Microsoft Access or ORACLE) that contains the normalised expression levels and a call as to whether the gene appears to be absent or present (Affymetrix only). This data is then associated in the relational database with annotation for known genes from various other DNA and protein databases. These databases includeEMBL (GenBank)<sup>TM</sup>, Swiss-Prot<sup>TM</sup>, TrEMBL<sup>TM</sup>, Incyte LifeSeq Gold® and the Derwent patent database. Information that is included is a description of the gene, keywords associated with that gene, tissue distribution and protein function annotation, HTML links to the online database entry, and an indication of the quality of the match between the gene on the microarray and the DNA/protein database entry as measured using Blast (version 2.0.8) statistics.

The data can be queried using the SQL query language in the relational database, where the information for the genes of interest can be extracted. This data can then be visualised using various data-mining software products including SpotFire on a personal computer and MineSet on a Silicon Graphics workstation. In addition to multi-dimensional visualisation, MineSet also has algorithms that can cluster genes according to, for example, similar expression profiles or tissue distributions.

## 20 Example 8: Functional Characterisation

This example describes how the gene sequences of the present invention can be further characterised with respect to protein structure the function, eosinophil biology and by inference function in other leukocytes.

#### Example 8.1: Delivery of antisense oligonucleotides to cell lines or primary cells

Antisense oligonucleotides of up to 20 nucleotides in length for any single gene sequence are designed as described previously along with an appropriate, inactive, control; oligonucleotides comprising the same nucleotide components but in a scrambled order or by inverting selected sequential oligonucleotides. These oligonucleotide sequences are additionally modified (e.g. methylphosphonate backbone or 2' methoxy modifications) for stability in the molecule. Oligonucleotides are resuspended in water at a concentration of 200µM . Oligonucleotides are delivered to cells in culture using commercially available lipids, for example Fugene 6 (Roche Molecular Biochemicals) or Superfect (Qiagen) or other , as per manufacturers instructions, or by using RPR proprietary lipids. Specifically oligonucleotides are diluted to the desired concentration (1-1000nM) and complexed with the lipid at the manufacturers recommended ratio.

Oligonucleotides are delivered to; primary human eosinophils, or other leukocytes, or other cell lines cultured in TF1-8 - RPMI-1640 with 10% heat inactivated FCS; 100U/ml penicillin and 100mg/ml streptomycin; 1mM sodium pyruvate and 2U/ml recombinant human IL-5 AML14.3D10 - RPMI-1640 with 10% heat inactivated FCS; 10μM β-mercapto ethanol and 1mM sodium pyruvate at 2-4x10<sup>5</sup> cells/ml then incubated at 37°C for up to 7 days. The impact of the antisense oligonucleotide on target gene transcription is assessed by quantitative PCR. RNA is prepared from transfected cells using the RNeasy miniprep kit (Qiagen) as per manufacturers instructions. Levels of target and an internal control mRNA are then determined using the TAQMAN technology as detailed below. The impact of the antisense oligonucleotide on target protein expression is assessed by Western blotting by standard procedures (Maniatis et al.(1989) in Molecular Cloning - A Laboratory Manual, CSH Laboratory Press) The impact of the antisense oligonucleotide on functional biology is described below.

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# Example 8.1.2: Retroviral delivery of gene sequences to cell lines or primary cells

Gene sequences in a sense or antisense orientation are delivered to cells of interest using either of two retroviral systems. The first system, the Phoenix MMLV system (Pear et al. (1993) Production of high-titer helper-free retroviruses by transient transfection. PNAS(USA) 90, 8392-6) utilises a Phoenix<sup>TM</sup> packaging cell line (cultured in DMEM + 10% heat inactivated FCS) in order to produce replicative-incompetent MMLV particles containing the gene of interest. The gene of interest is cloned into a packaging vector, for example pBMN (Pear et all (1993)) and transfected into the Phoenix packaging cell line by calcium phosphate precipitation. 20µg plasmid DNA is precipitated with calcium phosphate using the Promega Profection system as per manufacturers instructions. This precipitate is added to  $10^6$  cells in 3mls medium. Cells are incubated at 37°C for 5-7h, then the medium is changed and cells incubated for a further 24h. Medium is changed again and cells incubated for a further 48h. The supernatant is transferred to a 15 ml falcon tube and cellular debris removed by spinning at 800rpm for 5 minutes. The supernatant is then filtered through a 0.45mm filter, aliquotted in cryogen tubes and stored at - 80°C. The virus is then titred to assess the number of infectious particles. Target cells of interest are then infected with the viral particles at a suitable multiplicity of infection.(1-100) by adding the virus in a final volume of  $1 \, \mathrm{ml}$  to  $10^5$ cells in culture medium +  $8\mu g/ml$  polybrene. The cells and virus are then spun at 2500 rpm for 90 minutes at 32°C. Medium + 8µg/ml polybrene is added to a final volume of 2mls and cells cultured at 37° C overnight. The medium is then changed and cells incubated for a further 48h.Alternatively, the gene sequence of interest is introduced to target cells using a lentiviral

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system developed by Oxford Biomedica Limited (Kim et al. (1998) Minimal requirement for a lentivirus vector based on human immunodeficiency virus type 1 J. Virol. 72(1) 811-6). The sequence of interest is cloned into a lentiviral genome vector, for example pH4 or other and this plasmid is transfected using calcium phosphate precipitation as described into an efficient packaging cell line (293T cells) licensed from Standford University, together with vectors encoding accessory gag/pol and env proteins such as pGP-RRE3 and pRV67. Virus is then produced over a period of 72h as described for the Phoenix<sup>TM</sup> system. Viral particles encoding the gene of interest are harvested from the cell culture medium as described above then titred to assess the number of infectious particles. Target cells of interest are then infected with the viral particles at a suitable multiplicity of infection (1-100) as described above.

#### Example 8.1.3: Quantitation of Target mRNA Levels

Target mRNA levels are determined pre and post antisense oligonucleotide delivery to cells or cell lines by TaqMan (ABI PRISM 7700) quantitative RT-PCR analysis. Cytoplasmic RNA is isolated using the RNeasy 96 Kit (Quiagen) as per manufacturers instructions with the inclusion of the manufacturers recommendation regarding on column DNAse1 treatment. For each treatment, 10µl of the resulting RNA is reversed transcribed using the TaqMan Reverse Transcription Reagents Kit (PE Applied Biosystems) as per manufacturers instructions. 5µl of this is added to a 25µl final TaqMan PCR reaction mix (TaqMan Universal PCR Master Mix, as per manufacturers instructions). Target RNA quantitation is carried out using the relative standard curve methodology as described by PE Applied Biosystems and normalisation is carried out using a reference gene, for example GAPDH. Target RNA TaqMan primers/probe setss are designed using the PE Applied Biosystems Primer Express Software.

#### Example 8.2: Functional Assays

The impact of the genes described on functional biology of eosinophils, other leukocytes and model cell lines is evaluated by monitoring the impact of such genes on a number of functional biological and biochemical assays. Assays (for example adhesion, apoptosis, or calcium mobilisation) have been configured which are characteristic of the primary eosinophil or other leukocytes, in both primary eosinophils or other leukocytes per se, and in cell lines (for example AML14.3D10 (Baumann et al, Stem Cells, 1998;16;16-24), TF1.8(a gift from Prof. C. Sanderson, Institute for Child Health Research, Perth, Australia), HL60 (Tomonaga et al., Blood, 1986; 67:1433-1436) and EOL-1 (Mayumi, Leukemia and Lymphoma,1992; 7:243-250)). Potent antisense molecules that knockdown target mRNA

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levels are identified (see above) and transfected into an appropriate cell line, for example AML14.3D10, and a functional assay is performed (for example an adhesion assay or an apoptosis assay) at an appropriate time post transfection, for example 72 hours. Assays are performed with the appropriate scrambled control antisense oligonucleotide simultaneously, as an control. Similarly assays are carried out using cells in which candidate genes have been delivered in a sense orientation to evaluate over-expression or in an anti-sense orientation to identify any anti-gene effects.

#### Example 8.2.1: Adhesion assays

Adhesion assays are carried out using cells or primary eosinophils and looking at adhesion to a variety of substrates including plasma fibronectin (100µg/ml) cellular fibronectin (100µg/ml) coated on tissue culture plates, or to primary human endothelial cells. In a 96 well plate, 100µl of a 100µg/ml solution of fibronectin is added to each well, and equilibrated for one hour at 37°C. The wells are washed with PBS/1%BSA (bovine serum albumin) and then blocked non-specifically with a solution of PBS/1%BSA for one hour at room temperature. 2x10<sup>5</sup> cells in Puck's Buffer (Pucks Buffer (Sigma) /0.1%BSA / 2.5mM MnCl<sub>2</sub>) are bound to fibronectin coated plates or to confluent endothelial cells for one hour at 37 degrees celcius. Unbound cells are washed off (3 times) with RPMI containing 1% BSA and the bound cells lysed in mammalian lysis buffer (Promega) as per manufacturers instructions. Quantitation of bound cells is carried out using PicoGreen Nucleic Acid detection (Molecular Probes) as per manufacturers instructions. In this way genes are identified that enable or inhibit adhesion beyond the normal range and such genes are therefore implicated in the regulation of the adhesion process.

#### Example 8.2.2: Apoptosis Assays

Apoptosis assays are carried out using primary eosinophils or other leukocytes or cell lines including TF1.8 and AML cells. Apoptosis is monitored by caspase 3 activation or annexin V externalisation. Caspase 3 activation is measured using a CaspACE<sup>TM</sup> kit (Promega). Cells are harvested following antisense or retroviral treatment and pelletted by centrifugation (8000rpm for 5mins) Cell pellets are lysed using lysis reagent and caspase-3 enzyme activity monitored by production of a fluorescent substrate using a fluorescent plate reader as per manufacturers instructions. Annexin-5 is measured using the ApoAlert<sup>TM</sup> Annexin V apoptosis kit (Clontech). Cells are harvested following antisense or retroviral treatment and processed using an Annexin5 detection kit (Clonetech) as per manufacturers instructions. Cells are then fixed in 2% paraformaldehyde and analysed by flow cytometry.

#### Example 8.2.3: Chemotaxis assays

Chemotaxis assays are performed with eosinophils or other leukocytes or cell lines as described by King et al, J. Leuk Biol, 1997;62:465-8.

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#### Example 8.2.4: Activation Assays

In response to a range of stimuli eosinophils and leukocytes generally will be activated in a number of ways as specified below.

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#### Example 8.2.4.1: Eosinophil Peroxidase

EPO assays are performed for the measurement of EPO release in response to activation.  $5x10^5$  cells are incubated in HANK's buffer in the presence of activator, such as Histamine for one hour at  $37^{\circ}$ C. The supernatant is harvested and EPO concentration is determined by the method of Strah et al (J Immunol Meth, 1985; 83: 209-15).

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#### Example 8.2.4.2: Respiratory burst

This assay is carried out using lucigenin as a substrate Cells are cultured in a six well plate at  $5\times10^6$ /ml/well in standard medium. After a 24hr cells are washed three times in HBSS with calcium(Sigma +BSA (0.2%), HEPES (10mM), sodium bicarbonate (7.5%)) and seeded at  $5\times10^4$ /well into a white microlite microtitre plate containing pre-warmed lucigenin [50µM]. Cells are incubated for a further 30 minutes in a luminometer (ML3000 Microtiter Luminometer, Dynatech Laboratories) prior to addition of a prescribed stimulus at time zero.

# Example 8.2.4.3: CD69 Expression

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CD69 expression is employed as a marker of activation. 5x10<sup>5</sup>cells are incubated overnight in culture medium plus activator, for example Histamine. After overnight culture, the cell suspensions are centrifuged and the pellets are resuspended in cold RPMI-1640 (Sigma) and placed on ice for immunofluoresence staining and flow cytometry. This was performed as per Hartnell et al., Immunol, 1993; 80: 281-6.

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#### Example 8.2.4.1: Cystolic calcium

An elevation in cytosolic calcium is measured using a fluorescent calcium indicator dye such as Fura-2, Fluo-3, etc (Molecular Probes; Kao (1994) Meth Cell Biol 40 155-81) Calcium mobilisation assays on antisense treated or retrovirally targetted cells are carried out in two formats following loading of the cells with a fluorescent calcium indicator. For example cells in assay buffer [HBSS with calcium(Sigma +BSA (0.2%), HEPES (10mM), sodium

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bicarbonate (7.5%)]( are loaded with 3 $\mu$ M fluo-3 AM for 45min at 37 °C . Loaded cells are then washed three times and harvested into a 96-well plate (0.5 x10<sup>6</sup>/300 $\mu$ l). Agonists are micro-injected into the wells and change in fluorescence measured using the FLUOstar®(BMG Lab Technologies). Alternatively cells are monitored for changes in calcium in a Perkin Elmer dual excitation spectrophotometer using single assay cuvettes.

Other activation assays that may be employed to assess the impact of genes of interest include the use of a microphysiometer [Molecular Devices] to measure proton extrusion from the cell, eicosanoid production including prostaglandins and leukotrienes [measured in cell supernatants by ELISA or other immuno-assay]; and the production of known cytokines.

### Example 9: Antibody Production and Immunohistochemistry

Anti rabbit polyclonal peptide antibodies are produced to targets based on predicted peptide sequence and tested for their ability to react with protein via ELISA assay and by Western Blot using whole cell extracts (Maniatis et al (1989), in Molecular Cloning, A Lab Manual, CSH Laboratory Press, Second Edition). Reactive polyclonal antibodies are used to carry out immunohistochemistry on a wide range of human tissues and to compare the expression of a specified gene in diseased versus normal, tissues, for example in asthmatic lung versus normal lung or in any other inflammatory disease tissue.

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#### **CLAIMS:**

- 1. A polypeptide encoded by a polynucleotide according to any one of Seq ID Nos: 1-466 or a fragment the polypeptide.
- 2. A polypeptide variant having at least 90% amino-acid sequence identity to the polypeptide sequence of claim 1, and sharing at least one functional or structural characteristic with the polypeptide sequence of claim 1.
- 3. An isolated polynucleotide which encodes the polypeptide of claim 1 or 2.
  - 4. An isolated polynucleotide comprising the polynucleotide sequence of any one of Seq ID Nos: 1-466, or a fragment thereof.
- 5. An isolated polynucleotide variant having at least 90% polynucleotide sequence identity to one of the polynucleotides of claim 3 or claim 4.
  - 6. An isolated polynucleotide which hybridises under stringent conditions to one or more of the polynucleotides of claim 3, claim 4 or claim 5.
  - 7. An isolated polynucleotide which is complementary to one or more of the polynucleotides of claims 3 to 5.
- 8. A method of screening for agents which modify the activity of one or more of the polypeptides
  of claims 1 or 2, comprising the steps of a) exposing the polypeptide to at least one agent to be
  screened; b) detecting and/or measuring interaction and/or binding between the polypeptide and
  the agent.
  - 9. An agent identified according to the method of claim 8.
  - 10. An expression vector comprising one or more polynucleotides according to claims 3 to 7.
  - 11. An expression vector according to claim 10, wherein the polynucleotide is operatively associated with an expression control sequence which permits expression of the polynucleotide in a host cell.

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- 12. A host cell comprising an expression vector according to claim 10 or 11.
- 13. A method of producing a polypeptide encoded by any one of the polynucleotides of Seq ID Nos: 1-466, the method comprising the steps of a) culturing a host cell of claim 14 under conditions suitable for the expression of the polypeptide from the polynucleotide; and b) recovering the polypeptide from the host cell culture.
  - 14. A method of producing a polypeptide encoded by any one of the polynucleotides of Seq ID Nos: 1-466, the method comprising chemical synthesis.
- 15. A method of producing a polypeptide encoded by any one of the polynucleotides of Seq ID Nos: 1-466, the method comprising a) transforming an animal with an expression vector according to claim 10 or 11; and b) recovering the polypeptide from the transgenic animal.
- 16. A pharmaceutical composition comprising one or more of the polypeptides according to any of claims 1 to 2, and a pharmaceutically acceptable vehicle.
  - 17. A pharmaceutical composition comprising one or more of the polynucleotides, or fragments thereof, of claims 3 to 7 and a pharmaceutically acceptable vehicle.
  - 18. A pharmaceutical composition comprising a vector according to claim 10 or 11 and a pharmaceutically acceptable vehicle.
- 19. One or more polypeptides or fragments thereof according to claims 1 or 2, for use in the
   treatment of eosinophil mediated inflammatory disease.
  - 20. A pharmaceutical composition according to claim 16 for use in the treatment of eosinophil mediated inflammatory disease.
- 30 21. Use of one or more polypeptides or fragments thereof according to claims 1 or 2 in the manufacture of a medicament for treatment of eosinophil mediated inflammatory disease.
  - 22. Use of a pharmaceutical composition according to claim 16 in the manufacture of a medicament for treatment of eosinophil mediated inflammatory disease.

- 23. One or more of the polynucleotides, or fragments thereof, of claims 3 to 7 for use in the treatment of an eosinophil mediated inflammatory disease.
- 24. A pharmaceutical composition according to claim 23 for use in the treatment of eosinophil
   mediated inflammatory disease.
  - 25. Use of one or more of the polynucleotides, or fragments thereof, of claims 3 to 7, for use in the manufacture of a medicament for the treatment of eosinophil mediated inflammatory disease.

- 26. Use of a pharmaceutical composition according to claim 22 for manufacture of a medicament for treatment of eosinophil mediated inflammatory disease.
- 27. A pharmaceutical composition according to claim 18 for use in the treatment of eosinophilmediated inflammatory disease.
  - 28. Use of a pharmaceutical composition according to claim 18 in the manufacture of a medicament for treatment of eosinophil mediated inflammatory disease.
- 20 29. A purified antibody capable of binding to any one of the polypeptides of claims 1 or 2, or fragments thereof.
  - 30. A kit for diagnosis of disease characterised by inflammation, comprising means for assaying expression of a polynucleotide or polypeptide according to any one of claims 1 to 7 in a sample of eosinophils from a patient.
  - 31. A method of modulating apoptosis of eosinophil cells in a subject, comprising administering to the subject a polynucleotide according to any one of claims 3 to 7, wherein said polynucleotide sequence is operably linked to a regulatory sequence.

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32. A method of diagnosis of disease characterised by inflammation, the method comprising a) obtaining a sample of eosinophil cells from a patient; b) assaying said sample for levels of expression of a polynucleotide according to any one of claims 3 to 5.

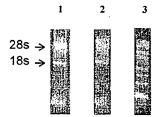
33. A method of diagnosis of a disease characterised by inflammation, the method comprising a) obtaining a sample of eosinophil cells from a patient; b) assaying said sample for levels of a polypeptide according to claims 1 or 2.

34. A method of inhibiting eosinophil migration in a subject, the method comprising
administering to the subject a polynucleotide sequence according to claim 6 or 7.

35. A transgenic, non-human animal comprising a recombinant polynucleotide having a sequence according to any one of claims 3 to 7.

36. An agonist or antagonist of the polypeptide of claims 1 or 2, wherein said polypeptide is a receptor.

Figure 1



Gel analysis of RNA isolated using the RNAzol modified methodology. (Lane:1 Eosinophils, Lane:2 Neutrophils, Lane:3 Molecular weight marker)

Figure 2

1Kb M cDNA

7 kb

Figure 3

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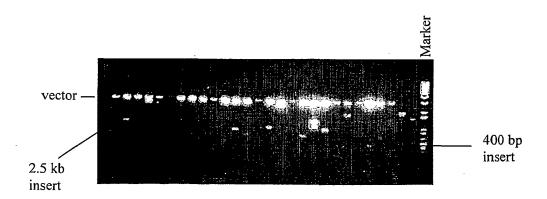


Figure 4

AscI

5' AAGCAGTGGTAACAACGCAGAA-GGCGCGCC-T(18) (A/G/C) 3'

NotI

5' AAGCAGTGGTAACAACGCAGAA -GCGGCCGC-GGG 3'

Figure 5

5' -	GGGCGCCCTTAATTAAG	- 3'
_		

3' - ACGTCCCGCGCGGAATTAATTCTTAA - 5'

#### SEQUENCE LISTING

<110> Aventis Pharmaceuticals Products Inc. <120> Polynucleotides and Polypeptides <130> 40/165/P/WO (CA2444 <140> <141> <160> 466 <170> PatentIn version 3.0 <210> 1 <211> 671 <212> DNA <213> Homo sapiens <400> 1 gggggagggg gccctcccgg gctggtgcag gtgcccggag gccccggggg ctcgcgcgtc 60 gcggcatcgg ggaagcggta gcaaccactc tcctcccgct ggctgcttct tacgactttt 120 cttttgttgt tgccgtgacc cgggtctgtt ttctcctctg ttgtttaagg tgttttcctg 180 ctgcaccggc tctgcgccct ccacctcctt ccctgtggtt ttaaccttcc tctttccccg 240 tgtgttttat gcacggcgaa ctacgtaaag atttgcattg cttccccact cggcaccccc 300 gececcaeet etetgaaaaa caaaaceeea aeeteacaaa aeetetatgg ateegeggta 360 gcgagacgtg aaggggttga tttgtggagt gggagttgct ggcccattgc ggtgcccggg 420 actcattaaa ctgtcactca cccccaccc cactgggtaa atggggtgat taatgtctga 480 tatattggaa tgggtcgagg gcatttgtgg agaataggtg gtgtggctgg gaagaaattg 540 atetecegag gatgteteet ggaetaagtg tteataatta tgteaeteae egegaagttg 600 gagaaagtta ggtttgtgac tttgggaaag cgagaaggac aggacggagt cgtcgggttt 660

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<211> 520

<212> DNA

<213> Homo sapiens

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<213> Homo sapiens

<212> DNA

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gaggaaacat gttgcaaatt ttctttatac tctgtcaagg gttttcctcg ggacacagct 240
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<210> 27

<211> 695

<212> DNA

<213> Homo sapiens

<220>

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<222> ()..()

<223> "n" is a single nucleotide whose identity could not unambiguously

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<210> 28

<211> 761

<212> DNA

<213> Homo sapiens

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<213> Homo sapiens

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cctcaaa	aaac	atttgttaat	tcctttgagt	gcaccnnnnn	nnnnnnnnn	nnnnnnnnn.	360
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tgtgacccag gtcctcagag gcacatgaaa aatgctaatg aacggcagca ctcattattc 480
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<211> 648

<212> DNA

<213> Homo sapiens

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<211> 434

<212> DNA

<213> Homo sapiens

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<211> 419

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<213> Homo sapiens

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tttttcaata	gtgatttatt	tcggtatata	tactttccaa	gaatgccacc	atttctaaat	360
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<211> 715

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<213> Homo sapiens

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<211> 619

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<213> Homo sapiens

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120

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<210> 47

<211> 405

<212> DNA

<213> Homo sapiens

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aggtcagtgt	tgtctgctac	acagectaet	ctctgtcttt	gggtgatttg	tctctctttg	360
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<212> DNA

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tgataattaa gtgtaagtt	g aactaatggt	tcaactttct	gacattagtt	aaaaaataaa	540
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<212> DNA

<213> Homo sapiens

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<211> 418

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<212> DNA

<213> Homo sapiens

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<210> 62

<211> 665

<212> DNA

## <213> Homo sapiens

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aaaagtgttg	aagtaggaag	gcctaagaga	aactaaagag	taactaccat	ctgatgatag	420
acctaaagcc	ctataactcc	cttcctctac	atgtatacac	acaccccaca	tagcacacaa	480
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<210> 64

<211> 659

<212> DNA

<213> Homo sapiens

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•

<210> 65

<211> 653

<212> DNA

<213> Homo sapiens

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ccttgtctc	t aaataaata	a agtgcataaq	g taattatta	t gttgttaga	g tataaataaa	540
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					atccagttct	240
	attcttcata					300
	: tttcctaaga					360
	gacaatgata					420
	catttcatcc					480
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<211> 647						
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	ccataagaag					240
	tgtggagtga					300
	gggagagcgt					360
					· · · · · ·	

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<211> 613						
<212> DNA						
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<u>/</u>						
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ttggcagctg	tttgtgaagt	cataagaaag	cgagtaaaga	ggtaatttat	taattagatt	360
gaaatattaa	atctattcct	tttttcccaa	gatactagtt	ttcccagaag	gtacttgtac	420
taatcgttcc	tgtttgatta	cttttaaacc	aggtgagaaa	aattaaatta	tgtattctaa	480
caaagtaata	tgtgagattt	tgcaaatgat	tttatagaaa	tacacaaaat	aactctttag	540
cttgctctga	gcatttttt	cttttctgat	agcaactttt	taacgttgtg	gatccacaga	600
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<210> 70

<211> 623

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> ()..()

<223> "n" is a single nucleotide whose identity could not unambiguously

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taaaggtagg	, taagattgtt	ttc				623
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<213> Hom	no sapiens					
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ccatcttcct	ccacttctca	cttcataaca	aggaggctgt	cacggaaaac	acccaaatga	420
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ccaggttgto	: tgtgaggtag	acctggtatc	tgaattcaag	taaagacctg	gaatacctca	540
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<210> 72		,				
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<213> Hon	no sapiens					
<220>						
<221> mis	c_feature					٠
<222> ().	. ()					
<223> "n"	' is a single	e nucleotid	whose idea	atity could	not unambig	iously

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gcacgo	gcac	ttccgccagt	ggtttcttcc	attgcctttg	ggatgagcag	gcctcctgaa	180
agcagg	rcctg	atattctctg	gtcttctgac	aaagaatggg	aaatttctca	caccgtcnnn	240
nnnnn	ınnnn	nncctgggga	tgggatttga	agggcttggg	ttgccgaatt	gctcctagaa	300
ccacag	gctt	agaggagttt	tctatgaaca	gcggtcctgg	cagggacaga	ctgaggatcg	360
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<211>	625						
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220>							
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222>	()	()					
223>	"n" j	is a single	nucleotide	whose iden	tity could m	not unambiguo	uslv

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aagagaatag aaatgtattc taacnnnnnn nnnnnnnnn nnnnnngtaa gagtgcccag 180
gggtattgag attgttagat tatttataa tgatataact taagggattc caaaataatg 240
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catattgtct	ttttttcttc	cccaatacta	tgagcgttag	agaatgagac	gcaaatccga	- 360
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tcctttttt	ttttcccaaa	aaata				625

<210> 74

<211> 736

<212> DNA

<400> 74

<213> Homo sapiens

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720

736

<210> 75

<211> 607

<212> DNA

<213> Homo sapiens

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<220>

<221> misc\_feature

<222> ()..()

<223> "n" is a single nucleotide whose identity could not unambiguously

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gtgcgcatag	ggctgtgcac	tgttgttcat	atgaggggct	gaagtgaggt	cataggtgtg	180
agaagcattt	acttggctac	aagtaaccnn	תתתתתתתתת	nnnttggaca	agcactgacg	240
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ctgaaccata	caaagatatt	cactgggggc	ccatcccctc	caggccctaa	aaatcatact	360
atttctcacc	ttcacactgt	gtaaccaccc	tctataacta	gaacatttgc	tagtetette	420
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cttgtaattc	agtcctcatg	tttaaattct	acacaaattt	aaatttaggg	tgttgagtgc	540
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atcattg						607

<210> 76

<211> 615

<212> DNA

<213> Homo sapiens

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tgctagtaga ggttacctga ccacaattag atatatctt gtactaacaa aatatgcaca 180
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WA 02/10100	DCT/CD01/0220
WO 02/10198	PCT/GB01/0339

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gctaccaatc	aatttttcc	ttttagaaag	aatgcataat	tttgatgaat	gctacagcaa	540
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tcatcacaat	atagc					615

<210> 77

<211> 403

<212> DNA

<213> Homo sapiens

<400> 77

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<210> 78

<211> 632

<212> DNA

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<220>

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<222> ()..()

<223> "n" is a single nucleotide whose identity could not unambiguously

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tgagag	tgcc	acttactatg	tttcatttgg	caggtgggtg	gggaacattt	aaaaccaaga	180
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gatata	gatg	gtatttaaaa	ctttaggaac	aaatgaaccc	acccaggaga	aggcccagaa	360
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ctgaga	aagt	gtggccaagt	tccatcctaa	ctttgtgtcc	attccctcca	cagtggatgg	480
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tgtttg	ttac	taataacag	ggcctattga	tagcagggct	ggagacaaag	ggaggggtgg	600
gtaggg	catt	tttgtctcta	gtatggcaag	tg			632
<210>	79						•
<211>	742						
<212>	DNA						
<213>	Homo	sapiens					

verso nomo saprens

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<210> 80
<211> 544
<212> DNA
<213> Homo sapiens
<220>
<221> misc feature
<222> ()..() ..
<223> "n" is a single nucleotide whose identity could not unambiguously
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                                                                     120
nnnnnnnnn nnnnnnnnn nncagctgtc catttttgcc tgctcttgtt tccctagtgc
                                                                     180
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ccagctctag ttgatctcag aaggggaatg tgggcacaaa ggaaggtctt ttaattatgg
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tcaa
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<211> 636
<212> DNA
<213> Homo sapiens
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	tgtaaacata					600
	agactgatag					636

<210> 82

<211> 570

<212> DNA

<213> Homo sapiens

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<210> 83

<211> 526

<212> DNA

<213> Homo sapiens

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tacaaaactt	aaaaaaaaa	ctttctggaa	ctaaaactga	gttttaaatt	taaaagttag	·240
taatgaattc	aaagaaagga	aaacgaagta	gaataaacat	caaaacagaa	acaatggggg	300
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gttttaccaa	cacacgcctg	tgctgtgtct	tttcaaaata	tcctaatggg	aactacaggg	420
atcttaagcc	aggaaaattc	acttctatcc	tttatcgctt	ctcttgctgc	ctccatctgt	480
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<210> 84

<211> 566

<212> DNA

<213> Homo sapiens

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cgcattgaga	ggaaggtgtc	tgccttaagg	taactggagg	ataaggctcc	gcccttccca	180
tgagagaggt	gctaactcac	tctcccacca	cacatcctgc	catccatcct	gactttggcc	240
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<210> 85

<211> 653

<212> DNA

<213> Homo sapiens

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caaato	aaag	accgggatgg	gttgagaagt	gaatggaatt	tgagcaactg	gagagaacaa	240
gcaaat	ttac	atgaactttg	gctgtgatag	taaggggagg	atgtagtagc	tgggtgctga	300
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aacagt	aagg	agtggggtga	tatctaaatg	ggtttctaag	ctggaagtga	actaacagag	540
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<212>	DNA				•		
<213>	Homo	sapiens					
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<220>

<221> misc\_feature

<222> ()..()

<223> "n" is a single nucleotide whose identity could not unambiguously

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atgategeea geagcattaa gagctatgtt tageetttat geeataetgt atettannn 180
nnnnnnnnn nncaaattet gaaacaaaac attaaaatgt gacteactee aaacagaaag 240

a	tggaaatgt	attcctacta	agaaatatgt	gtaacttcta	gaaaaagaaa	aaaaaaccca	300
C	agagatttg	ttttcaacat	attgtttttg	cttaagatat	atttttactc	ttaaaaatta	360
a	gaaatagaa	ggccttttat	tagaagcagt	gtagtgtcac	agaatgacaa	agcacagtat	420
C	agcagacag	aaaacgtggg	ttctaatctt	gctttcccta	cataactctc	aactggttat	480
ť	taggttctc	aataaagtag	aatgatgaaa	tacgtcttct	taatgctatt	gtattttgtt	540
a	atatttaac	actgttgata	tcaagatgag	atcttataag	tagctggaaa	actatcagtg	600
t	agggaaag						609

<210> 87

<211> 587

<212> DNA

<213> Homo sapiens

<400> 87 ggggaaaaaa aaaattcagt cgatttaaga taaaaagata ttcaagtagg caaataggtt 60 ttttaccatt ttttcctttt tgaatgttct aacattgttt agttaatcaa ctgataatca 120 tcatttatag gatccgagtt tcttacagcc taacagaaat gtgaaaagga tatttatagc 180 gaaacattat tttcccaact acaagagaaa atcaaatgaa gtaaacaaaa tttatgaaag 240 tttgctgtgc ttaatatgaa ttctccattg gtctgagaga tgatgctctc ctttctttgc 300 acagagtgaa agctagggta gaatttgggc aggaaataaa gaatagagca agatactgga 360 acttggggga aaaatctaac tcctcacggc tgaagtcttc ataattctgc atcagtgcca 420 cagtotacca gaaaccaggo cocotagtgg attaaaagag ttaaggactg aatgocacat 480 gagaatgatt tcaacactga ggttgtggaa attaaataca agaacgatat ttaattaaaa 540 atcttattca gtcactcatt tagcacttct ttttctttt ttcgaaa 587

<210> 88

<211> 589

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> ()..()

<223> "n" is a single nucleotide whose identity could not unambiguously

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<210> 89

<211> 573

<212> DNA

<213> Homo sapiens

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ctgggaatat	gaccgggaaa	attacaagta	aca	573

<210> 90

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<213> Homo sapiens

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cagtta	aaaa	caacaacaac	aacgacactc	acacattaca	ttttctgttt	ttctcagaat	540
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<210> 91

<211> 711

<212> DNA

<213> Homo sapiens

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<223> "n" is a single nucleotide whose identity could not unambiguously

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ttggaggtat	gtgggatagg	ttacagaaaa	tattccaaga	tgatatatga	gacatcttct	180
ccagaaacaa	aaatatgaat	tgcatttcat	ttctgtatta	caattcttag	tgctacagaa	240
tcacatgctg	ctcccaatgt	ctgcagggtc	aatggaagag	ccaaaaacca	tttaaannnn	300
nnnnnnnnn	nnnnnnnnn	nnnnnnnnn	nnnnnnntc	, ggaggtaaca	catatttcta	360
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acagtgccat	ggggcaccca	ggaaatgtct	gaatgttttg	ttaaaataag	tttaagagtt	600
gtctctgcqt	acaaggaact	gcctgtccac	tgaaagggtg	gcatgaattg	tgacttagaa	660
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<210> 92

<211> 652

<212> DNA

<213> Homo sapiens

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<210> 93

<211> 507

<212> DNA

<213> Homo sapiens

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<210> 94

<211> 515

<212> DNA

<213> Homo sapiens

<220>

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<222> ()..()

<223> "n" is a single nucleotide whose identity could not unambiguously

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cctcacctcg catctgtatc caccaatgaa gtcactgcat gttgccccgt gctggcaggg 180
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	/ GD01/03
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ggggttcaaa tcaaccaatg agcaagtaaa tctaaactgg ctgacacatc caatcttatt	420
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ccacgctttc taggccatga aaggagaggg gccctttccc tcgtgacccc agagcagatg	360
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cagtttagtt tctgataacc acttctcttt ctttgtctca tgtttccctt ccttcgtgaa	480
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Nomo Saprens	
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gcatgg	agcc	agttgatttc	ttaacatgca	ttggatcact	tttttcaggt	tacataaaga	180
tatagt <sup>.</sup>	tata	tttttcaaat	taagttttag	aaaaagacat	gtaaatgtga	gttaccttga	240
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tggtat	ccat	aagtatataa	atctatagta	ttataacatg	tctgatgata	atttatagta	360
gttggc	aatt	tgggnnnnnn	nı nnnnnnn	חחחחחחחחחח	ngttttcagt	attggctgag	420
taagct	cata	ctgaattgac	ccttctgcct	gtagagcagc	tctaaagtct	ggacacagga	480
ccaaaa	acga	ctatttgaag	gtagtggaac	gtgagcaaaa	ggaggcagga	gaacaggaga	540
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<213>	Homo	sapiens				·	
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<220>							
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actggaaggg aatgtgagct cattcttgga caaggttcaa ctactggaaa agcaattaat 180

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cataaccatg	catttgtata	ccaattttt	attttgctca	. tacaaatctg	tattgtaatg	540
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	-					
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72/265

<213> Homo sapiens

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gttttgaccc gtgattccgg ttttaaaggc tgagtagggc cgggcgcggt ggttcacctc	180
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<213> Homo sapiens	

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<223> "n" is a single nucleotide whose identity could not unambiguously

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<213> Homo sapiens

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tgtcatggct tgaacattca aaggggacct ccagttaaac aaggcagatc aaacacctct 360

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gtgaaccaca						180
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ttttcaagta a						300
gccaagcaca						360
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/CIJ/	TIOITO	aahreus				•	

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			cgtagccctg				360
			atccctggtg				420
			agacacacat				480
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ttc							. 603
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<210> 136

<211> 480

<212> DNA

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<210> 137

<211> 655

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> ()..()

<223> "n" is a single nucleotide whose identity could not unambiguously

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agcataaaag ctagatggcc tatgaaatgg actttgtaca aaagaaatgt ggcaactact 300

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<221> misc\_feature

<220>

<222> ()..(),

<223> "n" is a single nucleotide whose identity could not unambiguously

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gataaaatag	tgatcaccac	taaagacatg	taatacttat	ataacttaaa	tgtgcatcta	180
	taagcagttt					240
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<210> 140

<211> 595

<212> DNA

<213> Homo sapiens

<400> 140
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<213>	Homo sapiens					
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<221>	misc_feature					
<222>	()()					
<223>	"n" is a single	nucleotide	whose iden	tity could	not unambiguou	sly .

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<210> 142

<211> 409

<212> DNA

<213> Homo sapiens

<400> 142						
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gcagtgccag ggtactccct cettggcccc ttcctgctca actgctgtgg gtgacctgaa	360
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<212> DNA	

<220>

<221> misc\_feature

<213> Homo sapiens

<222> ()..()

"n" is a single nucleotide whose identity could not unambiguously

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tgggaatgcc	ctgatgccct	acatgcaagc	ctttgtgggc	gtctgtagga	cgctgtactg	420
gtctgcaact	gctaccacat	ctttaagctt	tctcctgtct	catgtatttt	cttcatttcc	480
catttggaat						490
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2011> E40				•		

<211> 549

<212> DNA

<213> Homo sapiens

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<210> 169

<211> 543 <212> DNA <213> Homo sapiens

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<210> 170

<211> 601

<212> DNA

<213> Homo sapiens

<220>

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<223> "n" is a single nucleotide whose identity could not unambiguously

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acttctcata tttctgaaat tttcaggaaa aaaaagtaga aaaaaactg cacctcaatc 180

tgtctgtaag	tttctattac	ttacttccca	gatcttcaat	ttgaggagat	gtcccccatc	240
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caatatgaat	aaccaaaaac	caaatgttaa	aaaaagagga	tccattttca	taacttagtg	420
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<210> 171

<211> 696

<212> DNA

<213> Homo sapiens

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<210> 172

<211> 413

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<213> Homo sapiens

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<223> "n" is a single nucleotide whose identity could not unambiquously

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180

nnnnnnnnn nncatgettt gttaatgtta acatactact getgetttta acattteatg

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<400> 178

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<220>
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<223> "n" is a single nucleotide whose identity could not unambiguously
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<213> Homo sapiens

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ttaactgagt	tgtttttgtt	ttttaaagg	aaagttgcat	caccaaatat	tttaaacatt	240

getgtggcaa tactaaatat teattataee aaaaacaatt eatteacaae ttgaacatet 300 tgtgtaagtt tteagatata taacatatat aeettttatt caaaaacaga aetgtggaat 360 tgtgttacet ttgttagtaa gacacateta geatgaaaae ettageaaaa tegtteagtg 420 atgtttagtg ttgaaataga tttetgttgt gttggaaaca taattgteta tttactagae 480 atagattaae tteattaae aaaagaaaat gtgggeeagg tgeta 525

<210> 188

<211> 619

<212> DNA

<213> Homo sapiens

í

<220>

<221> misc\_feature

<222> ()..()

<223> "n" is a single nucleotide whose identity could not unambiguously

<400> 188 taaaaaaaca tatgaaagta aaaaaaatct atgattaata ttctcataga gataagagaa 60 acatattcat aagcaagaag aggatataaa agttacattc agaaaacata aagcgctctt 120 gcaaattaaa aatgtgatag cagaaatgaa aaaattcaac aggcaagcta gaagaaggtg 180 tataatcatc tcagtaagta gagcaaaaac acaagagaga aaaaacgaga gaaagggtta 240 gataattaaa ggattaaccc aggcggttca atagctaaat agttcagaaa gaggataaag 300 360 aagatgaaaa tttcctaaaa ctaaagctag taggcattca gattttaagg gtgtgctaag 420 tgccaagcgc aataaaacaa aagaaaagaa caacaaaaaa actccttctc ataccaaagc 480 acagcagcat gaacatggag ataaaaagga cctaaaaggt cccagaaagt gaacaagtta 540 ccaacaggga gtgggagtcc acatgagaga tgtcagcagc agcactggaa gccacagggc 600 atggagcaat gatttcaaa 619

<210> 189

<211> 593

<212> DNA

<213> Homo sapiens

<400> 189 gggggtgaat agagcagggg caactgaagt tggctttcta atccaaacaa ttaqattaag 60 tgacagtgaa cataggaaag aacaaatatt tgctcagcct actgttaggc tctttqccaa 120 ctgctcccac gtggagactt agaaagccaa gtccaagaag gcgagatgat gccagacagc 180 tgcccagcaa gccctggccc caggtgctcg caaattccct ctctttgcat gggcagtatc 240 ctattccact ttgggaaaaa acaagagaaa ctgagaaagc caagggtatt ctgaagtatt 300 agaaagagat tagcactgtt taaccacaaa tgacaggaac tagggagaga ggaaqqccta 360 agagccagga tattctggca ggtactgtct taaaaatcata cattaaccag gtgctttgct 420 tctcaggtac taaatccatc tgggaacaca tacatcaacc taaaggccaa gtctctagag 480 atcccttccc aacgagettt ttctacccca tgctcccagt acacatgcaa aggettttgc 540 ttccactggg gaaaaaaaac aacaggaaac tcaagtagca ccgttccaca gca 593

<210> 190

<211> 535

<212> DNA

<213> Homo sapiens

<220>

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<223> "n" is a single nucleotide whose identity could not unambiguously

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aaacctgttt acttttacac gnnnnnnnn nnnnnnnnn nnnnnnnnn aaaatgtggt 180

cttctggtca tgtcgtttct taggatactc aggggaagcc agtcccatc tatatataat 240 agtcactgta ctgaaatgta aatttaaatc taatggcgaa ctagttaagt aacatttaa 300 tgaatatccg aagaagatgc aacagcaagt tagtttgata tcatcagaat ccaggtaaaa 360 agaaatacct gagaatccag caattattat taacaactct tttcccaatc ctttaatatt 420 tctgaaagaa taaaaataaa ctcttagcaa tggaaacggg tacccaagat aacagggata 480 gaagaaaatg tactcttacg agtctctgaa ttttgaatta tctcaatgta ttaac 535

<210> 191

<211> 614

<212> DNA

<213> Homo sapiens

<220>

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<222> ()..()

<223> "n" is a single nucleotide whose identity could not unambiguously

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<210> 192
<211> 621
<212> DNA
<213> Homo sapiens

<400> 192 ggggtctgga agagttaaaa acagctcaca ctgaccaagc tggttctctc tagtgaacag 60 ggtgtgggtg gtgcttatgt cagcagccca gggccatgtg tcaggggtgc caatgggcgg 120 agetgetggg etegatteet gtggtttgge accaeagett gaettgettt ggetttgatt 180 cttttcacac actgagetca ggttctcact gtctccttta cctcccacct caactcacat 240 ttaccaagee teactgtgga ectggetaca gggatgggea gagtgttagg geateaceee 300 gggtcctgga ttgtgtgagg gcgttacctc ccaagagaaa cctgcttgca accatgtgcc 360 aggecagetg etgtgagaaa eeettetett agtecagaga agtttgtgea etttaettae 420 ttagactete ettttetete tetetettt ttttttttt tttgagatgg ggteteetgg 480 cacttgcttt tcttttaata tagaaataga tattgggatg ctatatgcac atattaaaat 540 atatggatgt tgaagagcaa gaggaaaagg agaaacttga gtaaagaatg cttggactgg 600 gccaggcgcg gtggcttcag a 621

<210> 193

<211> 481

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> ()..()

<223> "n" is a single nucleotide whose identity could not unambiquously

<400> 193
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CCCCCa	aaga	cacatgtgac	ccaccacccc	atctctgatg	tgtctctcac	agcttgaaaa		180
gcctga	gaca	gctgtcttgt	gagggactgn	nnnnnnnn	nnnnnnnnn	nncccctttg		240
tgactt	caag	agcctctggc	atctctttct	gcaaaggcac	ctgaatgtgt	ctgcgtccct		300
gttago	ctgt	ctcaacttta	tgtgcactga	gctgcaactt	cttacttccc	tgctgaaaat		360
aagaat	ctga	atatcaattt	gttttctcaa	atatttgcta	tgagaggttg	atggattaat		420
taaata	agtc	aattcctgga	atttgagaga	gcaaataaag	açctgagaac	cttccagaaa		480
a								481
<210>	194							
<211>	722						\	
<212>	DNA						,	

<213> Homo sapiens

<400> 194 agaagcaagt gatgttaatc aagagaatat atttattaca aagtaaaaat tcagacaaaa 60 ctagaattca atcaaaaata tttagatgta agaaagtcat tggaaaaagg agtatgtgtt 120 aacaaaagac tttttaaaat aaatcggtca ttaaacgtct tagtattgtg caactctaag 180 aacatgtgag aataagaaaa aaggaggaaa acaatctttt aaaaccatgt cagatgatta 240 agctagcaaa cagtgaatca tgtctagtta tattgcattc aagttctagc tcttgttagt 300 catttatttt aaattaaagc atcaaaggag ttcaaaagtt gacatgcaca caaaaaaatt 360 gtgggaactc agcccagtta cacccactct acattaccta agatatgagt gaagcaggta 420 ccgagagtct taattaatgc ataggtatga ggcaacaagg aattcttaat tatgaagact 480 gagatgcaaa aaagcaaaaa cttagccaaa atagttcact ataaaatatc tacataattt 540 ggaaaagggt ctctttttt ttttttttt caatatatag tggttttaat tttcgtttac 600 tacatccaaa gtaagaaata tttttacatt ataacccaac aaacatttca tgaaacatta 660 tttaccttta ctacatgtta tagatgtgta tgtttcctat ttcttccttt ttttgtttta 720 tg 722

<210> 195

<211> 451

<212> DNA

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<210> 196

<211> 457

<212> DNA

<213> Homo sapiens

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<210> 197

<211> 469

<212> DNA

<213> Homo sapiens

<400> 197

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caaagetttt teacatetgg accateagag aagagatget etettteaac aaagagetgt	360
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taatatgtaa geetgeacae tteaetetae taagttteea etgggtetga gttattetgg	120

115/265

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<210> 200

<211> 654

<212> DNA

<213> Homo sapiens

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<210> 201

<211> 477

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> ()..()

<223> "n" is a single nucleotide whose identity could not unambiguously

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<210> 202

<211> 432

<212> DNA

<213> Homo sapiens

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PCT/GB01/03390

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<222> ()..()

<223> "n" is a single nucleotide whose identity could not unambiguously

<400> 204 ggttggaagg gttattgcag agaccatttt aaggtcaagc gactgccagg ttttcagaca 60 ggcagtggtt tgtttctgta cttatctgga taaccaagga gaacaatctc agggagggtg 120 gctaaacagg aattcttttg cacctttcca cctctttta tttcttctc tctcccnnnn 180 240

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<210> 205

<211> 727

<212> DNA

<213> Homo sapiens

<400> 205
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accaactage attettet gataagagac caccaaccat agagggatte tgtccagtca 180

caaatcccca tettgttett teetteetea aagtgtttgt ttetagette tgaccagagg 240

caatgettee caggetgtea gtatggeace etgeatgeaa caaccettaa tgagaaataa 300

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taaaggaaag aggtatatac agaatatgga aacattgtgt gggattgaat aaagtagaag 420

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<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

<400> 210

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<223> "n" is a single nucleotide whose identity could not unambiguously

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1

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<211> 727

<212> DNA

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<211> 690

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<213> Homo sapiens

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360

420

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<223> "n" is a single nucleotide whose identity could not unambiguously

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<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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gctaaq	gaagc	tacaaagaat	gacgggaaac	actctaactg	cagggtttgc	aagtactatc	420
ccccc	jcctc	accccccctt	cttttctttg	ataggcagaa	<sup>l</sup> ygaaataaaa	taaatagacc	480
*		ttagctccag					540
cttgac	tgct	gagagtgcta	tactggtgaa	aatgtaggtc	agcccaagca	ggcagcagtt	600
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<400> 248
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caacctgggt cacagcaggc ccaggaccct ggaagctgag ctcccctata tgggaaagga 180
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<223> "n" is a single nucleotide whose identity could not unambiguously

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cctgctcagc tttcaccttc c	cagcgttacc	tggagcaacc	ctgtggggag	ctgtaggctg	420
tccccataga cttctgagat g	gtctttcttt	ctctccatct	gcaggaagat	gtcagagece	480
cagtettttc cetaggagag g	gcttccctag	atggtgggag	tcctggccca	ggccactgtg	540
ggttttacga agttgaaggt o	cctggttcgg	tgatggcaca	ggggcacaca	taataacttc	600
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<210> 249

<211> 520

<212> DNA

<213> Homo sapiens

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<223> "n" is a single nucleotide whose identity could not unambiguously

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atatgataga	taaagggaca	gaatatactt	accaggagcc	aataacccaa	cggtctacta	180
tcataatccg	gcagatctgg	agcaatctta	caagcttgta	tgttcaggta	tttaaatatg	240
tggactatgc	cttttataca	tatctaaata	aagtcacaca	gatgtagcca	aattattact	300
catctgaagt	atgctccttt	ttatcatatc	aacattttat	gtaacataca	ttgggaaagg	360
gaggcatttc	tatcaagtac	atacagtgnn	nnnnnnnnn	nnnnnnnn	nnnnnnngg	420
ttaagtgtta	ttttaggtgt	ttaactggta	aatatgtttt	cattttctag	tcactaatac	480
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<210> 250

<211> 632

<212> DNA

<213> Homo sapiens

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<210> 251

<211> 670

<212> DNA

<213> Homo sapiens

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		gggccaggtt				180
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cctgcc	tccc	aggetecage	catcggctaa	caggtcgagg	atgcttgtcc	cgagcagggt	300
gcctac	aggg	tgccaatgac	atttacaaag	aactgttctg	caacagtcta	ctatgaacat	360
actgga	aggc	tggacaggca	ggggacgatg	gacagaccgc	agcttttctg	caggacgtgg	420
gcagag	ctgg	agaggcccta	caacgttctg	tgccactgcg	gtcacctcca	tcgtactccg	480
ccttcc	cctg	ccaccacagg	acctggatgc	aaagacaccc	ccaaagacct	aaagtgtggg	540
tgagat	ggac	aagtcatggt	gcatctgaac	aaatcagccc	gcagcgatca	gatactatgg	600
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<220>

<221> misc\_feature

<222> ()..()

<223> "n" is a single nucleotide whose identity could not unambiguously

<400> 254 gggagcctta gcctgctcct ccctacccat tacccaatgt aagttgtaag gcaactgttg 60 gctagaagaa aggateteaa eccaetgttt etgeeeteac caageeetgt ettgetagee 120 atetetgece teaaccette ttagtetetg caatgtteag tgaaaactee ceagacacag 180 cagtttgcgt gtgtgagggg agaggaagtc ccaaggctgg ggctgggcca ggtgggacct 240 ggtgctttgc aacagcatcc catttgacca cagttaggtt ttgaccctga tgggaggagc 300 agatggaggg aggcatcagt ttaaagtggg gaagtggaat gggnnnnnnn nnnnnnnnn 360 ctcagaagga ggctttcagc ctttccttgc tagttcctgc taactgtctt cttgctcaga 420 ggagggtagg gaagcatgtg tgcaactggg ttgggaggtg gggtggatgt caccaggcag 480 gggtgcattg atttgttgaa gaaggcagca tatgaggcct ggcagtggga cagttggagg 540

WO 02/10198				PCT/C	GB01/03390
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<211> 674				·	
<212> DNA					
<213> Homo sapiens					
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agcccaccag aagctattga					120
tttccatgac tgcccgcagc		1			180
aaggagcagg tgccatggta					240
cttacagcga cgacaagcct					300
agtctcctgg ctcaccttgg	cctcatcatt	ccgaaggcca	tcactgccac	catgctgttc	360
aggaacatgg taggataagg	tgacgaggct	tggaggcctt	tgggtgtcca	cttgagttca	420
cgtggggaac tctgggttcc	aggatcgctc	ttcagagatc	tgaacacctg	tgttttcttt	480
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acagaagage ceteggagea	atcttggaag	caccccctgg	cctcagtgct	cgctgttcca	600
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<210> 256					
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-					
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ccccacataa aagcacatcc	caatagaaag	acaaaacatt	acaggggcca	aacactacca	240

300

360

gaagcaagtt taacaacttc gtgccccaaa gcccttgcct ctccccagct taactaccta

ggtatcaacg gaagagagc aagagttgtg ttaagacact ctccattcaa agaacaaaat

ggtgaaagtc ccaaagagtc ctgttctcta gtgacttgta ggttcgtgca taaaacgaag	420
actgtggtta catacaaagc cttatgttcc agaaggactg ataatgaagt aaggaaatgg	480
tgctccagcc atctgtgtta ataagcactt ggttttcaac ttgatcatta tcttatggat	540
aaatatettg caggeagtte tgtagtttte attaggggat gettaaggea aaaggtaget	600
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<212> DNA	
<213> Homo sapiens	
<400> 257 .	
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aataggtctg gagatttcaa gtgaggcatt tgcaaaacaa gatgggaggg agcagactga	180
agcagggacc ctgggaaacg tgaggcaccc tgggagaagt gggggaccaa ggaggaaagg	240
agataggcag gaaactettg geteetgtea ateateaaaa eeatggaaag teeeagaaag	300
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atcccaaatt tcctctctcc attccaccca caaatatgcc tctcttcata gttcagcaaa	480
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			gtttgggaaa			300
			tgaagatccc			360
			gagctggcca			420
			gtcctgactg		•	480
			tcaaagaact			540
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<210> 259

<211> 630

<212> DNA

<213> Homo sapiens

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<210> 260

<211> 705

<212> DNA

<221> Homo sapiens
<220>
<221> misc\_feature
<222> ()..()

<223> "n" is a single nucleotide whose identity could not unambiguously

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<210> 261

<211> 483

<212> DNA

<213> Homo sapiens

<220>

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<222> ()..()

<223> "n" is a single nucleotide whose identity could not unambiguously

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cgaatt	ggga	tccaaacaag	ctccagaaca	aaggactaac	agactactgc	tttgactata	180
accctc	ccga	tgaaaaccag	attgtgggac	accaggtcat	tctgtacctc	tgtcatggga	240
tgggcc	agaa	tcagttttc	gagtacacgt	cccagaaaga	aatacgctat	aacacccacc	300
agcctg	agnn	nnnnnnnnn	nnnnnnnag	gaatggatac	ccttatcatg	catctctgcg	360
aagaaa	ctgc	cccagagaat	cagaagttca	tcttgcagga	ggatggatct	ttatttcacg	420
aacagt	ccaa	gaaatgtgtc	caggctgcga	ggaaggagtc	gagtgacagt	ttcgttccac	480
tct							483
<210>	262						
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<400> 262
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aggcacaaat gagctcgcga ggcccnnnnn nnnnnnnnn nnnnnnnnn ggaggggaat 180
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<223> "n" is a single nucleotide whose identity could not unambiguously

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	tgagtttggt acacttgagt ccttctttga	240
	agctgatgtc tgaactctag gccatggcgc	300
	gggaactttc ctctgctact ttcatctcca	360
	aagccctaga gatgttatat ttatagtcag	420
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<211> 574		
<212> DNA		
<213> Homo sapiens	•	
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ggggttagac aggtaccggt cagactacgg		180
ccggtcagat tacggtggca caggcggcgt		240
tggcacaggc ggcgtggggt tagacaggta		300
is so	ccyyrcagar racggrggca caggeggegt	360

ggggttagac	aggtaccggt	cagattacgg	tggcacaggc	ggcgtggggt	tagacaggta	420
ccggtcagat	tacggtggca	caggcggcgt	ggggttagac	aggtaccggt	cagattacga	480
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cacggcgatc	ttgggtgagc	gacagaacaa	gttactctct	gaaccccagt	taatagaatg	360
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ccaaataatt	aacaaaagc	acatcaacag	aagagataaa	cagaagagat	taaaaacaca	180
aatattotoa	atgattctca	ctcaaaaaga	ttctagaaac	cataaaatgt	ataagccact	240
ataataactc	agaaggcagt	gtgacaagaa	aaaaattagg	attaaqcatq	cagattaatg	300

gacgtatttg aactggaaat aatcattttt agatatcctc attatcaaac tatatgagtt	360
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ccggcgggga caggggcagg gtgtactcag atgaatgagg cacagtctgt gcctctcaca	180
gccagatggc agaggcagac acagaaatcc atcatttcaa catgaagtgg cagaggggag	240
atacggggcc attggggctg caggacccag cctggtgggc agcggcagct tctaggaggg	300
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360

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	· capacing					
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<211> 811

<212> DNA

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<213> Homo sapiens

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<213> Homo sapiens

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<211> 440

<212> DNA

<213> Homo sapiens

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<211> 557

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<213> Homo sapiens

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<213> Homo sapiens

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<210> 362

<211> 712

<212> DNA

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<220>

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<222> ()..()

<223> "n" is a single nucleotide whose identity could not unambiquously

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<213> Homo sapiens

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WO 02/10	198				PCT	/GB01/03390
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218/265

<211> 572

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<213> Homo sapiens

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<213> Homo sapiens

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<213> Homo sapiens

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PCT/GB01/03390 WO 02/10198

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WO 02/10198	PCT/GB01/03390

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420

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<210> 461

<211> 642

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> ()..()

<223> "n" is a single nucleotide whose identity could not unambiguously

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tattttaact aaaatgcaac ttannnnnn nnnnnnnnn nnaatatatt tatgaaacat 180

VΖ

agcagaatta ccaaaa	aaag attgtcaatt t	ttcctaagtt	aaatgtaagg	atgcaaatgt	240
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<210> 462

<211> 609

<212> DNA

<213> Homo sapiens

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<211> 723

<212> DNA

<213> Homo sapiens

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<220>

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<211> 414

<212> DNA

<213> Homo sapiens

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cctaacctct	tctccctctg	gattcctgag	aacccttcct	tctttctggt	tctgtgggcc	180
				tgcaacgaca		240
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